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"Examiner Search Notes"

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James Martinell
Primary Examiner 1631

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OM nucleic - nucleic search, using sw model

Run on: November 29, 2003, 17:02:55 ; Search time 106 Seconds
(without alignments)
6891.406 Million cell updates/sec

Title: US-09-700-696C-1

Perfect score: 1655

Sequence: 1 gtgaataaagaatatagatat.....ataaaaaaaaaaaaaaaaaa 1655

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:*

- 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
- 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
- 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
- 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
- 5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|---------|-----------------------|--------------------|
| c 1 | 70 | 4.2 | 7218 | 1 US-08-232-463-14 | Sequence 14, Appli |
| 2 | 48 | 2.9 | 2277 | 1 US-08-676-967-2 | Sequence 2, Appli |
| 3 | 48 | 2.9 | 2277 | 1 US-08-676-974-2 | Sequence 2, Appli |
| 4 | 48 | 2.9 | 2277 | 2 US-09-098-487-2 | Sequence 2, Appli |
| 5 | 42.2 | 2.5 | 2621 | 2 US-08-553-619B-8 | Sequence 8, Appli |
| 6 | 39.6 | 2.4 | 696 | 3 US-09-461-697-193 | Sequence 193, App |
| 7 | 39.6 | 2.4 | 699 | 3 US-09-461-697-191 | Sequence 191, App |
| 8 | 39.6 | 2.4 | 717 | 3 US-09-461-697-189 | Sequence 189, App |
| 9 | 39.6 | 2.4 | 774 | 3 US-09-461-697-187 | Sequence 187, App |
| 10 | 39.6 | 2.4 | 819 | 3 US-09-461-697-185 | Sequence 185, App |
| 11 | 39.6 | 2.4 | 1869 | 3 US-08-461-697-184 | Sequence 184, App |
| 12 | 39.2 | 2.4 | 719 | 3 US-08-714-918-11 | Sequence 11, Appl |
| 13 | 39.2 | 2.4 | 719 | 3 US-09-265-315-11 | Sequence 11, Appl |
| 14 | 39.2 | 2.4 | 719 | 3 US-09-265-315-11 | Sequence 11, Appl |
| 15 | 39.2 | 2.4 | 719 | 3 US-09-266-417-11 | Sequence 11, Appl |
| 16 | 39.2 | 2.4 | 1850 | 3 US-08-617-860B-32 | Sequence 32, Appl |
| 17 | 39.2 | 2.4 | 2447 | 2 US-09-014-963-14 | Sequence 14, Appl |
| 18 | 39.2 | 2.4 | 4098 | 2 US-08-605-106-4 | Sequence 4, Appli |
| 19 | 38.6 | 2.3 | 1605 | 4 US-09-369-247-18 | Sequence 18, Appl |
| 20 | 38 | 2.3 | 273 | 4 US-09-134-001C-132 | Sequence 132, App |
| 21 | 38 | 2.3 | 2007 | 2 US-08-743-637B-169 | Sequence 169, App |
| 22 | 38 | 2.3 | 2007 | 3 US-08-526-840B-169 | Sequence 169, App |
| 23 | 38 | 2.3 | 2028 | 4 US-09-134-001C-1710 | Sequence 1710, App |
| 24 | 38 | 2.3 | 2422 | 1 US-07-867-106-5 | Sequence 5, Appli |
| 25 | 38 | 2.3 | 3138 | 1 US-07-867-106-4 | Sequence 4, Appli |
| 26 | 38 | 2.3 | 5852 | 1 US-07-867-106-2 | Sequence 2, Appli |
| c 27 | 37.8 | 2.3 | 1830121 | 4 US-09-557-884-1 | Sequence 1, Appli |

| | | | | | |
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| c 28 | 37.8 | 2.3 | 1830121 | 4 US-09-643-990A-1 | Sequence 1, Appli |
| 29 | 37.6 | 2.3 | 1293 | 4 US-09-370-838-219 | Sequence 219, App |
| 30 | 37.4 | 2.3 | 3527 | 4 US-08-909-965C-7 | Sequence 7, Appli |
| 31 | 37.2 | 2.2 | 1474 | 3 US-08-821-994-64 | Sequence 64, Appli |
| 32 | 36.8 | 2.2 | 1038 | 4 US-09-560-419-4 | Sequence 4, Appli |
| 33 | 36.8 | 2.2 | 2673 | 4 US-09-336-447A-12 | Sequence 12, Appli |
| 34 | 36.4 | 2.2 | 1134 | 4 US-09-328-352-3017 | Sequence 3017, App |
| 35 | 36.4 | 2.2 | 4285 | 4 US-09-410-464-1 | Sequence 1, Appli |
| 36 | 36.4 | 2.2 | 1664976 | 4 US-08-916-421B-1 | Sequence 1, Appli |
| 37 | 36.2 | 2.2 | 681 | 4 US-09-134-001C-2725 | Sequence 2725, App |
| 38 | 36.2 | 2.2 | 870 | 5 PCT-US95-13658-3 | Sequence 3, Appli |
| 39 | 36.2 | 2.2 | 11288 | 3 US-08-646-301A-1 | Sequence 1, Appli |
| 40 | 36.2 | 2.2 | 11288 | 4 US-08-481-968A-4 | Sequence 4, Appli |
| 41 | 36.2 | 2.2 | 11288 | 4 US-08-154-7112B-4 | Sequence 4, Appli |
| 42 | 36.2 | 2.2 | 15056 | 4 US-09-474-699-10 | Sequence 10, Appli |
| 43 | 36.2 | 2.2 | 30549 | 4 US-09-134-001C-322 | Sequence 322, App |
| c 44 | 36.2 | 2.2 | 1664976 | 4 US-08-916-421B-1 | Sequence 1, Appli |
| c 45 | 36 | 2.2 | 1219 | 4 US-08-195-705-1 | Sequence 1, Appli |

ALIGNMENTS

RESULT 1
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 INMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZgpt-F1s
US-08-232-463-14

Query Match 4.2%; Score 70; DB 1; Length 7218;

Db 394 ACNGTNTTYGNCARTTYGGGNCNGNTYNGARGTNAAYATHCCNMGNNAARCCNGAYGN 453
QY 466 GATATATCTCTTTCAGTGGGACGCCCAACCTTTTAAGGACATTCCTGGTAAAGAGAGAA 525
Db 454 AARATGNGGNTT---YGGNTTYGNCARTTYAARAYVYNTYNGARCCNGNNAARGN 510
QY 526 GCTACTGTCCTGACCTAGAACGCAAGATATTCACAGGGTTTTCAGCGCCCAAGTGAA 585
Db 511 YTNAAGGNGATGAAYATGAARGARATHAARGGNMGNACNGTNGTNGAYTGGGNGTGN 570
QY 586 GCTGAGAGTACTCATCTTGACACAAAGAGCCAGGTTATAATGAGATCCACAGAGAGAA 645
Db 571 GCAARGAYATYAARGAYACNARWSNGTNGNWSNAGTNGGARGARARWSNCA 630
QY 646 GAAATATGTTGGAAATACCAATTGGAACTAGGGATGAACTCGAAGAGGACAGATGCTGTT 705
Db 631 GARWSNARCAICARGARWSNGTNAARAARAARGGNMGNARGARGARGAYATGGARGAR 690
QY 706 GATGTCAGCTTGTAGAGGCGACGACGATATCATGCGGTAGTACCAATTTTAAGGAGCTC 765
Db 691 GARGARAAYGAYGAYGAYGAYGAYGAYGAYGAYGARGAYGNGTNTTYGAYGAYGAR 750
QY 766 CTTGAAGAGAGGAAACAGTGGATGCTGCGAGCCAAATGCTCACCAAGGAGGTT 825
Db 751 GAYGARGARGARGARAYATHGARWSNARGTNAACNARCCNGTNCARATHCARARWGN 810
QY 826 GATGTTCAATTCCTCTGACCTCAACCTCAAGAGAGAAAGAGAGAGGAGTGTATGCA 885
Db 811 GCGTNAARWNGNCCNGCNCNGCNAARWSNNGAYCAYWSNARGARGAYWSNGAYTN 870
QY 886 GCTGAAGTACCAACTATATGAAATTCCTAAATGCGCAAGGCGAGTACCAGAAAGGT 945
Db 871 GARGARWSNGAYWSNATHGAYGAYGNGARGARYTNGCNCARWSNGAYACNWSNACNGAR 930
QY 946 GTAGATCAATCTTAATAGGACCAAGCAACCTTAATGAAAGGAGGTTTCTCTAGTAA 1005
Db 931 GARGARGAYARCCNGTNCARGTNGWSNAYARABARARWGNARNTNCCNWSNGAY 990
QY 1006 GCGAA 1010
Db 991 GTNAA 995

RESULT 5

US-08-553-619B-8
; Sequence 8, Application US/08553619B
; Patent No. 5919705
; GENERAL INFORMATION:
; APPLICANT: DeHaan, Petrus T.
; TITLE OF INVENTION: Virus Resistant Plants
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; STREET: 975 California Avenue
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/553,619B
; FILING DATE: December 1, 1995
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Marcus-Wyner, Lynn
; REGISTRATION NUMBER: 34,869
; REFERENCE/DOCKET NUMBER: 137-1082/PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/354-3588

; TELEFAX: 415/857-1125
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2621 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; ORIGINAL SOURCE:
; ORGANISM: Chimeric tomato spotted wilt virus S RNA
US-08-553-619B-8

Query Match 2.5%; Score 42.2; DB 2; Length 2621;
Best Local Similarity 54.1%; Pred. No. 0.14; Mismatches 0; Gaps 0;
Matches 86; Conservative 0; Indels 73; Indels 0; Gaps 0;

QY 1497 TAAGCAAAAAAATCAITACAGATCTATGAAATAGGTAACATTTGAGTAGGTGTCATTT 1556
Db 667 TATAATATATAAGCTTCTTTAICTTTATTGCTTGTGCTTGTGTTAAATTT 726

QY 1557 AAAATAGTGTGTAATGTCAAAATGCTTCTATGTTGTTGCTCTGTAGACATGAAA 1616
Db 727 TAAATAAGTGTGTTAAATTAAGTTTGTCTTCTGTGTTGCTTTAAATAATAAATAA 786

QY 1617 TAAACAATATCTCTCGATGATAAAAAAATAAAAAA 1655
Db 787 TAACAAAAACAACGAAACAAAAATAATAATAATAA 825

RESULT 6
US-09-461-697-193
; Sequence 193, Application US/09461697
; Patent No. 6277974
; GENERAL INFORMATION:
; APPLICANT: COGENT NEUROSCIENCE, Inc.
; APPLICANT: Lo, Donald C.
; APPLICANT: Barney, Shawn
; APPLICANT: Thomas, Mary Beth
; APPLICANT: Portbury, Stuart D.
; APPLICANT: Purnam, Kasturi
; APPLICANT: Katz, Lawrence C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
; TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING
; TITLE OF INVENTION: CELL DEATH
; FILE REFERENCE: 10001-005-999
; CURRENT APPLICATION NUMBER: US/09/461,697
; CURRENT FILING DATE: 1999-12-14
; NUMBER OF SEQ ID NOS: 466
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 193
; LENGTH: 696
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-461-697-193

Query Match 2.4%; Score 39.6; DB 3; Length 696;
Best Local Similarity 43.6%; Pred. No. 0.37;
Matches 177; Conservative 0; Mismatches 229; Indels 0; Gaps 0;

QY 517 AAAGGAGAAAGTACTGCTCTGACCTAGAGGCAAGATATTCAAACAGGTTTGACGGC 576
Db 268 AAAGGGAGCTGGAAAGAGACAAAGATGAAAGGGGAGAGATGGAAGAGAGGAT 327

QY 577 CCAAGTGAAGCTGAGAGTACTCATTTGACACAAAAAACCCAGGTTTATATGAGATCCCA 636
Db 328 AAAAATGGAATGAGAAAGGAGAGATGCAAAAGAGAAAGATGGAAGGAGGTTGAA 387

QY 637 GAGAGAGAGAAATGCTGGAATACCATTTGGAACCTAGGGATGAACTGCGAAGAGGCA 696
Db 388 GACGGAAAGGAAATGGAAGATGGAAGAGAGAGAGAGATGAAAGAGAGAGAA 447

QY 697 GATGCTGTTGATGTCAGCCCTTGTAGAGGCGACACGATATCATGCTGTTAGTACCAATTT 756
Db 448 GACAGAAAGAAACACAGGAGCTTGGAAAGAGAGATGAAGATGGAAGAGAGAGAGATAA 507

| | | | |
|----|-----|--|-----|
| Qy | 757 | AAGGACCTCCCTGGAAAGAGAGGAAGCAACAGAGTGGATGCTGGCAGCCAAAATGCTCACCA | 816 |
| | | | |
| Db | 508 | AAAGAGGGGAAGATGTTAAAGTCAAGAAAGATGAAAAGAGAGAGATGGAAGA | 567 |
| | | | |
| Qy | 817 | GGGAAGTTTGAGTTTCATTACCTCTCTGCACCTCAAAAGAGAAAAGAGAGGCGAGT | 876 |
| | | | |
| Db | 568 | GATGAAGGTGGAAATGAGGAAGAGCTGGAAAAGAGAAAGAGATTTAAAAGAGAGGAA | 627 |
| | | | |
| Qy | 877 | AGTGATGCAGCTGAAAGTACCAACTATATAGAAATTCCTTAAAAATG | 922 |
| | | | |
| Db | 628 | GAAGGAAAAGAGCAAGATGAGATCAAAAGAGATGATGGAAGAAAAG | 673 |
| | | | |

RESULT 7
US-09-461-697-191
; Sequence 191, Application US/09461697
; Patent No. 6277974
; GENERAL INFORMATION:
; APPLICANT: COGENT NEUROSCIENCE, Inc.
; APPLICANT: Lo, Donald C.
; APPLICANT: Barney, Shawn
; APPLICANT: Thomas, Mary Beth
; APPLICANT: Portbury, Stuart D.
; APPLICANT: Puranam, Kasturi
; APPLICANT: Katz, Lawrence C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
; TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING
; TITLE OF INVENTION: CELL DEATH
; FILE REFERENCE: 10001-005-999
; CURRENT APPLICATION NUMBER: US/09/461,697
; CURRENT FILING DATE: 1999-12-14
; NUMBER OF SEQ ID NOS: 466
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 191
; LENGTH: 699
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-461-697-191

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RESULT 8
US-09-461-697-189
; Sequence 189, Application US/09461697
; Patent No. 6277974
; GENERAL INFORMATION:
; APPLICANT: COGENT NEUROSCIENCE, Inc.
; APPLICANT: Lo, Donald C.
; APPLICANT: Barney, Shawn
; APPLICANT: Thomas, Mary Beth
; APPLICANT: Portbury, Stuart D.
; APPLICANT: Puranam, Kasturi
; APPLICANT: Katz, Lawrence C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
; TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING
; TITLE OF INVENTION: CELL DEATH
; FILE REFERENCE: 10001-005-999
; CURRENT APPLICATION NUMBER: US/09/461,697
; CURRENT FILING DATE: 1999-12-14
; NUMBER OF SEQ ID NOS: 466
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 189
; LENGTH: 717
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-461-697-189

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RESULT 9
US-09-461-697-187
; Sequence 187, Application US/09461697
; Patent No. 6277974
; GENERAL INFORMATION:
; APPLICANT: COGENT NEUROSCIENCE, Inc.
; APPLICANT: Lo, Donald C.
; APPLICANT: Barney, Shawn
; APPLICANT: Thomas, Mary Beth
; APPLICANT: Portbury, Stuart D.
; APPLICANT: Puranam, Kasturi
; APPLICANT: Katz, Lawrence C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
; TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING

```
; TITLE OF INVENTION: CELL DEATH
; FILE REFERENCE: 10001-005-999
; CURRENT APPLICATION NUMBER: US/09/461.697
; CURRENT FILING DATE: 1999-12-14
; NUMBER OF SEQ ID NOS: 466
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 187
; LENGTH: 774
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-461-697-187

Query Match      2.4%; Score 39.6; DB 3; Length 774;
Best Local Similarity 43.6%; Pred. No. 0.39;
Matches 177; Conservative 0; Mismatches 229; Indels 0; Gaps 0;

QY 517 AAAGGAGAACTACTGCTCCTGACCTAGAGGCAAGATATTCACACAGGGTTTCAGGC 576
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 346 AAAGGGGAAGCTGGAAAGAGACAAAGATGAAAGAGGGGAGAGATGGAAAGAGAT 405
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 577 CCAAGTGAAGCTGAGAGTACTCATCTTTGACACAAAAAGCCAGGTTTATATGAGATCCCA 636
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 406 AAAAAATGGAATGAGAAAGAGAGATGCAAAAAGAGAAAGATGGAAAAAGGTGAA 465
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 637 GAGAGAGAAATGTTGGAATACCATTTGACACAAAAAGCCAGGTTTATATGAGATCCCA 696
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 466 GACGGAAGGAAATGAGAGAGATGGAAGAGAGAAAGAGAGAGATGAAAAAGGAGAA 525
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 697 GATCCTGTGATGTCAGCTTGTAGAGGCGCAGCAACGATATCATGGGTAGTACCAATTTT 756
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 526 GACGAAAGAAACAGAGATTGGAAAGAGATGAAAGATGAAAGAGAGAGAGAGATGAA 585
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 757 AAGGAGCTCCTGGAAGAGAGAAACAGAGTGGTCTGCGAGCCCAAAATGCTCACAA 816
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 586 AAAGGAGGAAAGATGTAAGAGTCAAGAGATGAAAGAGAGAGAGATGGAAGAGAA 645
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 817 GGGAGGTTGAGTTTCATTACCTCCTGACCCCTCAAGAGAGAAAGAGAGAGAGAGT 876
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 646 GATGAAGGTGGAATGAGGAGAGAGCTGGAAGAGAGAAAGAGAGATTTTAAAGAGAGAA 705
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 877 AGTGATGAGCTGAAAGTACCAACTATATGAAATTCCTTAAAAATG 922
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 706 GAAGGAAAGAGGAGATGAGATCAAGAGATGATGAAAAAAG 751
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 10
US-09-461-697-185
; Sequence 185, Application US/09461697
; Patent No. 6277974
; GENERAL INFORMATION:
; APPLICANT: COGENT NEUROSCIENCE, Inc.
; APPLICANT: Lo, Donald C.
; APPLICANT: Barney, Shawn
; APPLICANT: Thomas, Mary Beth
; APPLICANT: Portbury, Stuart D.
; APPLICANT: Puranam, Kasturi
; APPLICANT: Katz, Lawrence C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
; TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING
; TITLE OF INVENTION: CELL DEATH
; FILE REFERENCE: 10001-005-999
; CURRENT APPLICATION NUMBER: US/09/461.697
; CURRENT FILING DATE: 1999-12-14
; NUMBER OF SEQ ID NOS: 466
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 185
; LENGTH: 819
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-461-697-185

Query Match      2.4%; Score 39.6; DB 3; Length 819;
Best Local Similarity 43.6%; Pred. No. 0.4;
Matches 177; Conservative 0; Mismatches 229; Indels 0; Gaps 0;

QY 517 AAAGGAGAACTACTGCTCCTGACCTAGAGGCAAGATATTCACACAGGGTTTCAGGC 576
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 470 AAAGGGGAAGCTGGAAAGAGACAAAGATGAAAGAGGGGAGAGATGGAAAAAGAGAT 529
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 577 CCAAGTGAAGCTGAGAGTACTCATCTTTGACACAAAAAGCCAGGTTTATATGAGATCCCA 636
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 530 AAAAAATGGAATGAGAAAGAGAGATGCAAAAAGAGAGAGATGGAAGAGAGATGGA 589
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 637 GAGAGAGAAATGTTGGAATACCATTTGAAACTAGGGATGAAATTCGGAAGAGGCA 696
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 590 GACGGAAGGAAATGAGAGAGATGGAAGAGAGAAAGAGAGAGATGAAAAAGAGAA 649
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RESULT 11
US-09-461-697-184
; Sequence 184, Application US/09461697
; Patent No. 6277974
; GENERAL INFORMATION:
; APPLICANT: COGENT NEUROSCIENCE, Inc.
; APPLICANT: Lo, Donald C.
; APPLICANT: Barney, Shawn
; APPLICANT: Thomas, Mary Beth
; APPLICANT: Portbury, Stuart D.
; APPLICANT: Puranam, Kasturi
; APPLICANT: Katz, Lawrence C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
; TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING
; TITLE OF INVENTION: CELL DEATH
; FILE REFERENCE: 10001-005-999
; CURRENT APPLICATION NUMBER: US/09/461.697
; CURRENT FILING DATE: 1999-12-14
; NUMBER OF SEQ ID NOS: 466
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 184
; LENGTH: 1669
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-461-697-184

Query Match      2.4%; Score 39.6; DB 3; Length 1669;
Best Local Similarity 43.6%; Pred. No. 0.55;
Matches 177; Conservative 0; Mismatches 229; Indels 0; Gaps 0;

QY 517 AAAGGAGAACTACTGCTCCTGACCTAGAGGCAAGATATTCACACAGGGTTTCAGGC 576
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 470 AAAGGGGAAGCTGGAAAGAGACAAAGATGAAAGAGGGGAGAGATGGAAAAAGAGAT 529
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 577 CCAAGTGAAGCTGAGAGTACTCATCTTTGACACAAAAAGCCAGGTTTATATGAGATCCCA 636
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 530 AAAAAATGGAATGAGAAAGAGAGATGCAAAAAGAGAGAGATGGAAGAGAGATGGA 589
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RESULT 12

US-08-714-918-11/c

; Sequence 11, Application US/08714918

; Patent No. 6037123

; GENERAL INFORMATION:

; APPLICANT: Benton, Bret

; APPLICANT: Lee, Ving

; APPLICANT: Malouin, Francois

; APPLICANT: Martin, Patrick K.

; APPLICANT: Schmid, Molly B.

; APPLICANT: Sun, Dongxu

; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS ANTIBACTERIAL

; TITLE OF INVENTION: TARGET GENES

; NUMBER OF SEQUENCES: 111

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon

; STREET: 633 West Fifth Street

; CITY: Suite 4700

; STATE: Los Angeles

; COUNTRY: California

; COUNTRY: U.S.A.

; ZIP: 90071-2066

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; MEDIUM TYPE: storage

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: IBM P.C. DOS 5.0

; SOFTWARE: Word Perfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/714,918

; FILING DATE: September 13, 1996

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 60/009,102

; FILING DATE: December 22, 1995

; APPLICATION NUMBER: 60/003,798

; FILING DATE: September 15, 1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Warburg, Richard J.

; REGISTRATION NUMBER: 32,327

; REFERENCE/DOCKET NUMBER: 222/005

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (213) 489-1600

; TELEFAX: (213) 955-0440

; TELEX: 67-3510

; INFORMATION FOR SEQ ID NO: 11:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 719 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; US-08-714-918-11

Query Match

2.4%; Score 39.2; DB 3; Length 719;

Best Local Similarity 56.1%; Pred. No. 0.48;

Matches 74; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

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QY 1549 TGTCAATTTAAAAATAGTTGGTGAATGTCACAAATGCTTCTATGTTGTTGCTCTGTAGA 1608
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RESULT 13

US-09-265-315-11/c

; Sequence 11, Application US/09265315

; Patent No. 6187541

; GENERAL INFORMATION:

; APPLICANT: Benton, Bret

; APPLICANT: Lee, Ving J.

; APPLICANT: Malouin, Francois

; APPLICANT: Martin, Patrick K.

; APPLICANT: Schmid, Molly B.

; APPLICANT: Sun, Dongxu

; TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS

; TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS

; NUMBER OF SEQUENCES: 111

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon

; STREET: 633 West Fifth Street

; CITY: Suite 4700

; STATE: Los Angeles

; COUNTRY: California

; COUNTRY: U.S.A.

; ZIP: 90071-2066

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; MEDIUM TYPE: storage

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: IBM P.C. DOS 5.0

; SOFTWARE: Word Perfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/265,315

; FILING DATE: March 9, 1999

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/714,918

; FILING DATE: September 13, 1996

; APPLICATION NUMBER: 60/009,102

; FILING DATE: December 22, 1995

; APPLICATION NUMBER: 60/003,798

; FILING DATE: September 15, 1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Warburg, Richard J.

; REGISTRATION NUMBER: 32,327

; REFERENCE/DOCKET NUMBER: 240/247

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (213) 489-1600

; TELEFAX: (213) 955-0440

; TELEX: 67-3510

; INFORMATION FOR SEQ ID NO: 11:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 719 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; US-09-265-315-11

Query Match

2.4%; Score 39.2; DB 3; Length 719;

Best Local Similarity 56.1%; Pred. No. 0.48;

Matches 74; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

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| Db | 318 | GAGTATAAAAGCACTTGTGCAAAACACAAAGTGTCTTAAACTTAATTTATTGTTCACT | 259 |
| QY | 1609 | CATGAAATATAA | 1620 |
| Db | 258 | AGTTGAATCAA | 247 |

Search completed: November 29, 2003, 18:15:24
 Job time : 110 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 29, 2003, 18:13:30 ; Search time 535 Seconds
(without alignments)
10191.985 Million cell updates/sec

Title: US-09-700-696C-1

Perfect score: 1655

Sequence: 1 gtaataagaataatagatat.....ataaaaaaaaaaaaaaaaaa 1655

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2190069 seqs, 1647345023 residues

Total number of hits satisfying chosen parameters: 4380138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| 1 | 1638 | 99.0 | 1876 | 12 | US-09-794-422-33 Sequence 33, Appl |
| 2 | 1638 | 99.0 | 1969 | 12 | US-09-794-422-45 Sequence 45, Appl |
| 3 | 1638 | 99.0 | 2019 | 12 | US-09-794-422-5 Sequence 5, Appl |
| 4 | 1638 | 99.0 | 2112 | 12 | US-09-794-422-7 Sequence 7, Appl |
| 5 | 1369 | 82.7 | 1662 | 12 | US-10-311-840-3 Sequence 3, Appl |
| 6 | 1289 | 77.9 | 1575 | 12 | US-10-311-840-2 Sequence 2, Appl |
| 7 | 514.8 | 31.1 | 1655 | 12 | US-09-794-422-1 Sequence 1, Appl |
| 8 | 485.2 | 29.3 | 1682 | 12 | US-09-794-422-3 Sequence 3, Appl |
| 9 | 60 | 3.6 | 60 | 12 | US-09-794-422-3 Sequence 16013, A |
| 10 | 47.6 | 2.9 | 3673778 | 12 | US-10-312-841-1 Sequence 1, Appl |
| 11 | 46.8 | 2.8 | 345 | 12 | US-09-814-353-5466 Sequence 5466, Ap |
| 12 | 46.8 | 2.8 | 345 | 12 | US-09-814-353-11753 Sequence 11753, A |
| 13 | 46.5 | 2.8 | 2826 | 12 | US-10-032-585-6930 Sequence 6930, Ap |
| 14 | 45.8 | 2.8 | 2000 | 10 | US-09-887-576-831 Sequence 831, App |
| 15 | 44.8 | 2.7 | 3673778 | 12 | US-10-312-841-2 Sequence 2, Appl |
| 16 | 44.6 | 2.7 | 349 | 12 | US-09-814-353-18039 Sequence 18039, A |

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| 17 | 44.6 | 2.7 | 637 | 12 | US-10-027-632-244151 | Sequence 244151, |
| 18 | 44.6 | 2.7 | 637 | 12 | US-10-027-632-244152 | Sequence 244152, |
| 19 | 44.6 | 2.7 | 637 | 13 | US-10-027-632-244151 | Sequence 244151, |
| 20 | 44.6 | 2.7 | 637 | 13 | US-10-027-632-244152 | Sequence 244152, |
| C 21 | 44.4 | 2.7 | 5218 | 12 | US-10-311-455-1239 | Sequence 1239, Ap |
| C 22 | 44.4 | 2.7 | 14006 | 12 | US-10-311-455-1931 | Sequence 1931, Ap |
| C 23 | 44.2 | 2.7 | 403 | 12 | US-09-814-353-17949 | Sequence 17949, A |
| C 24 | 44.2 | 2.7 | 8530 | 12 | US-10-311-455-1727 | Sequence 1727, Ap |
| C 25 | 44.2 | 2.7 | 21537 | 12 | US-10-311-455-1971 | Sequence 1971, Ap |
| C 26 | 44 | 2.7 | 6155 | 12 | US-10-340-453-235 | Sequence 235, App |
| C 27 | 44 | 2.7 | 9997 | 12 | US-10-311-455-342 | Sequence 342, App |
| C 28 | 44 | 2.7 | 9997 | 12 | US-10-311-455-342 | Sequence 38, Appl |
| C 29 | 43.6 | 2.6 | 341 | 10 | US-09-960-352-12302 | Sequence 12302, A |
| C 30 | 43.4 | 2.6 | 631 | 12 | US-09-814-353-5993 | Sequence 5993, Ap |
| C 31 | 43.4 | 2.6 | 631 | 12 | US-09-814-353-12272 | Sequence 12272, A |
| C 32 | 43.2 | 2.6 | 7634 | 12 | US-10-311-455-2103 | Sequence 2103, Ap |
| C 33 | 43.2 | 2.6 | 8962 | 12 | US-10-311-455-2103 | Sequence 659, App |
| C 34 | 43 | 2.6 | 65 | 12 | US-09-908-975-111 | Sequence 111, App |
| C 35 | 43 | 2.6 | 6587 | 12 | US-10-311-455-358 | Sequence 358, App |
| C 36 | 43 | 2.6 | 10377 | 12 | US-10-311-455-2193 | Sequence 2193, Ap |
| C 37 | 42.8 | 2.6 | 5204 | 12 | US-10-311-455-872 | Sequence 872, App |
| C 38 | 42.8 | 2.6 | 5369 | 12 | US-10-311-455-525 | Sequence 525, App |
| C 39 | 42.8 | 2.6 | 7703 | 12 | US-10-311-455-1408 | Sequence 1408, Ap |
| C 40 | 42.8 | 2.6 | 11729 | 12 | US-10-311-455-868 | Sequence 868, App |
| C 41 | 42.8 | 2.6 | 32195 | 14 | US-10-102-627-92 | Sequence 92, Appl |
| C 42 | 42.6 | 2.6 | 747 | 12 | US-10-140-472-212 | Sequence 212, App |
| C 43 | 42.6 | 2.6 | 747 | 12 | US-10-141-761-212 | Sequence 212, App |
| C 44 | 42.6 | 2.6 | 747 | 12 | US-10-142-885-212 | Sequence 212, App |
| C 45 | 42.6 | 2.6 | 747 | 12 | US-10-158-790-212 | Sequence 212, App |

ALIGNMENTS

RESULT 1

US-09-794-422-33
; Sequence 33, Application US/09794422
; Publication No. US20030166239A1
; GENERAL INFORMATION:
; APPLICANT: Brown, Thomas A.
; APPLICANT: De Wet, Jeffrey R.
; APPLICANT: Gowen, Lori C.
; APPLICANT: Hames, Lynn M.
; TITLE OF INVENTION: Mammalian Osteoregulins
; FILE REFERENCE: PC10445
; CURRENT APPLICATION NUMBER: US/09/794,422
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 60/185,617
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 60/234,500
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33
; LENGTH: 1876
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-794-422-33

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| Query Match | 99.0% | Score 1638; | DB 12; | Length 1876; |
| Best Local Similarity | 100.0%; | Pred. No. 0; | | |
| Matches 1638; | Conservative 0; | Mismatches 0; | Indels 0; | Gaps 0; |
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| QY | 62 | TTTATCTTAAGTCACTGGGAATAAGGGTTTGAGATGAGATGATCTATCAGCAAC | 121 | |
| Db | 299 | TTTATCTTAAGTCACTGGGAATAAGGGTTTGAGATGAGATGATCTATCAGCAAC | 358 | |
| QY | 122 | TACATGACCAAGAAGAAATATGGCGAGCTCTCATCGAATAACATGCAACATATATGG | 181 | |

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Db 419 GGCAGTGAATCGGATTAATACTCTGGGGAAGAGAAACAAAGAGAAACACACCTAGGAATG 478
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Qy 302 AGCTCAAGAGATTCCTCAAGCCAGCAAGAGTCCAGTAAAGCAAAAGCACCACATCGTA 361
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Db 779 TAGAAGGCAAGATATTCAACAGGGTTTGAGCCCAAGTGAAGCTGAGAGTACTCATC 838
Qy 602 TTGACACAAAGACCCAGGTTATATGAGATCCAGAGAGAGAGAAATGGTGAATA 661
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Db 1019 ACAGATGGATGCTGGCAGCCAAATGCTCACCAAGGAGAGGTTGAGTTTCATTACCTC 1078
Qy 842 CTGCACCTCAAAAG 901
Db 1079 CTGCACCTCAAAAG 1138
Qy 902 ATAATGAAATTCCTAAAG 961
Db 1139 ATAATGAAATTCCTAAAG 1198
Qy 962 GGAACCAAGCAACCTTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1021
Db 1199 GGAACCAAGCAACCTTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1258
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Db 1259 TGCCCATCTCTCTCGTGGTCTTGATATGAATCAAAAGAGAGAGAGAGAGAGAGAGAGAG 1318
Qy 1082 GCGGAGTCATGAGATATATACATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1141
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Qy 1142 AAAATAATTCACAGGAATAGGATGTCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1201
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Qy 1262 GTGCGAGTTCAAGTGAAGCGATGGTGAATAGTCCACAGAGAGTTCCAGCGGGGTGACA 1321
Db 1499 GTGCGAGTTCAAGTGAAGCGATGGTGAATAGTCCACAGAGAGTTCCAGCGGGGTGACA 1558
Qy 1322 GTCTGAAGACCTCGTCAACCTGTGAGTTGATGTAGAGAGAGCCACCTGACAGCTGACAG 1381
Db 1559 GTCTGAAGACCTCGTCAACCTGTGAGTTGATGTAGAGAGAGCCACCTGACAGCTGACAG 1618
Qy 1382 GTGAAGAGAGATAGAGTGAAGAACTGAGTGAAGCAAGTCTCTGGTCTCTCTGGGGGAA 1441
Db 1619 GTGAAGAGAGATAGAGTGAAGAACTGAGTGAAGCAAGTCTCTGGTCTCTCTGGGGGAA 1678
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RESULT 2

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; Sequence 45, Application US/09794422
; Publication No. US20030166239A1
; GENERAL INFORMATION:
; APPLICANT: Brown, Thomas A.
; APPLICANT: De Wet, Jeffrey R.
; APPLICANT: Gowen, Lori C.
; APPLICANT: Hames, Lynn M.
; TITLE OF INVENTION: Mammalian Osteoregulins
; FILE REFERENCE: PC10445
; CURRENT APPLICATION NUMBER: US/09/794,422
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 60/185,617
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 60/234,500
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45
; LENGTH: 1969
; TYPE: DNA
; ORGANISM: Homo sapiens
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Query Match 99.0%; Score 1638; DB 12; Length 1969;
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Matches 1638; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1172 CTGCAACCTTCAAAAGAGAGAGAGAGAGGAGGAGTGTGATGAGCTGAAAGTACCAACT 1231
Qy 902 ATAATGAAATTCCTAAATGCGAAGGAGTACAGAAAGGAGTGTGATGATTCATA 961
Db 1232 ATAATGAAATTCCTAAATGCGAAGGAGTACAGAAAGGAGTGTGATGATTCATA 1291
Qy 962 GGAAACCAAGCAACCTTAAATGAAAGCAAAAGGTTTCTAGTAAAGGCAAAAGTCAAGGCC 1021
Db 1292 GGAAACCAAGCAACCTTAAATGAAAGCAAAAGGTTTCTAGTAAAGGCAAAAGTCAAGGCC 1351
Qy 1022 TGCCCATTCCTTCTCGTGGTCTTGATAATGAAATCAAAACGAAATGGATTCTTTAATG 1081
Db 1352 TGCCCATTCCTTCTCGTGGTCTTGATAATGAAATCAAAACGAAATGGATTCTTTAATG 1411
Qy 1082 GCCCAGTCATGAGAAATATAAACAATGCGAGAAATATCATTTATGTACCCCAAGAC 1141
Db 1412 GCCCAGTCATGAGAAATATAAACAATGCGAGAAATATCATTTATGTACCCCAAGAC 1471
Qy 1142 AAAATAATTTCTACGGAATAAGGTTATGCCACAGGGAAGGCTCCTGGGTGAGCAAC 1201
Db 1472 AAAATAATTTCTACGGAATAAGGTTATGCCACAGGGAAGGCTCCTGGGTGAGCAAC 1531
Qy 1202 CCCATTCCAAGAGGTTTATTCTCCGTAGAGGGATGACAGTATGAGTATCTTGACA 1261
Db 1532 CCCATTCCAAGAGGTTTATTCTCCGTAGAGGGATGACAGTATGAGTATCTTGACA 1591
Qy 1262 GTGGCAGTTCAAGTACAGCGATGTTGACTAGTCCACAGAGGATTCACAGCGGGGTGACA 1321
Db 1592 GTGGCAGTTCAAGTACAGCGATGTTGACTAGTCCACAGAGGATTCACAGCGGGGTGACA 1651

RESULT 3

US-09-794-422-5

; Sequence 5, Application US/09794422

; Publication NO. US20030166239A1

; GENERAL INFORMATION:

; APPLICANT: Brown, Thomas A.

; APPLICANT: De Wet, Jeffrey R.

; APPLICANT: Gowen, Lori C.

; APPLICANT: Hames, Lynn M.

; FILE REFERENCE: PCI0445

; CURRENT APPLICATION NUMBER: US/09/794,422

; CURRENT FILING DATE: 2001-02-27

; PRIOR APPLICATION NUMBER: 60/185,617

; PRIOR FILING DATE: 2000-02-29

; PRIOR APPLICATION NUMBER: 60/234,500

; PRIOR FILING DATE: 2000-09-22

; NUMBER OF SEQ ID NOS: 46

; SOFTWARE: Patent in Ver. 2.0

; SEQ ID NO 5

; LENGTH: 2019

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-794-422-5

Query Match 99.0%; Score 1638; DB 12; Length 2019;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1638; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TGAATAAAGATATAGTATCAGTAAACAAGAGAACTCAACAATGGCCTGAGGATGTCAA 61
Db 382 TGAATAAAGATATAGTATCAGTAAACAAGAGAACTCAACAATGGCCTGAGGATGTCAA 441
Qy 62 TTATCTCTAAAGTCAACTGGGAATAAAGGGTTTGGAGATGGAGATGATGCTATCAGCAAC 121
Db 442 TTATCTCTAAAGTCAACTGGGAATAAAGGGTTTGGAGATGGAGATGATGCTATCAGCAAC 501
Qy 122 TACATGACCAAGAAGATATGGCGAGCTCTCATCAGAAATAACATGCAACATATAATGG 181
Db 502 TACATGACCAAGAAGATATGGCGAGCTCTCATCAGAAATAACATGCAACATATAATGG 561
Qy 182 GSCCAGTGCCTCGGATTAACCTCCCTGGGGAAGAAAACAAAGAGACACACCTAGGAATG 241
Db 562 GSCCAGTGCCTCGGATTAACCTCCCTGGGGAAGAAAACAAAGAGACACACCTAGGAATG 621
Qy 242 TTCTAAAACATAATCCCAAGCAAGTATGAATTATGCTAAAGCACACTCGAAGGATAAAGA 301


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QY 422 TTGAAGCAGCGGTTATACAGATCTTCAAGAGAGGGGACAAATGATATATCTCCTTTCA 481
Db 714 TTGAAGCAGCGGTTATACAGATCTTCAAGAGAGGGGACAAATGATATATCTCCTTTCA 773
QY 482 GTGGGACAGCGCAACCTTTTAAAGACATCTCTGTAAAGAGAGACTACTGTGCTGACC 541
Db 774 GTGGGACAGCGCAACCTTTTAAAGACATCTCTGTAAAGAGAGACTACTGTGCTGACC 833
QY 542 TAGAAGCGAAAGATATTTCAACAGGGTTTTCAGGCCCAAGTGAAGCTGAGAGTACTCATC 601
Db 834 TAGAAGCGAAAGATATTTCAACAGGGTTTTCAGGCCCAAGTGAAGCTGAGAGTACTCATC 893
QY 602 TTGACACAAAAAAGCCAGGTTTATAATCAGATCCAGAGAGAGAGAAATGGTGGAAATA 661
Db 894 TTGACACAAAAAAGCCAGGTTTATAATCAGATCCAGAGAGAGAGAAATGGTGGAAATA 953
QY 662 CCATTGGAACCTAGGATGAAATGCGGAAAGAGGAGATGCTGTGATGTGAGCCTTTAG 721
Db 954 CCATTGGAACCTAGGATGAAATGCGGAAAGAGGAGATGCTGTGATGTGAGCCTTTAG 1013
QY 722 AGGCGACACGATATCATGGTAGTACCAATTTTAAAGGAGCTCCCTGGAGAGAGGAA 781
Db 1014 AGGCGACACGATATCATGGTAGTACCAATTTTAAAGGAGCTCCCTGGAGAGAGGAA 1073
QY 782 ACAGAGTGGATGCTGGCAGCCAAATGCTCAACAGGGAAGGTGAGTTTCATTACCCCTC 841
Db 1074 ACAGAGTGGATGCTGGCAGCCAAATGCTCAACAGGGAAGGTGAGTTTCATTACCCCTC 1133
QY 842 CTGCACCTCAAAGAGAAAGAAAGAGCGAGTAGTATGAGCTGGAAGTACCAACT 901
Db 1134 CTGCACCTCAAAGAGAAAGAAAGAGCGAGTAGTATGAGCTGGAAGTACCAACT 1193
QY 902 ATATGAAATTCCTAAATGGCAAGGAGTACCAAGAGGAGTGTAGTCAATCTTAATA 961
Db 1194 ATATGAAATTCCTAAATGGCAAGGAGTACCAAGAGGAGTGTAGTCAATCTTAATA 1253
QY 962 GGAACCAAGCAACCTTAAATGAAACCAAGAGGTTTCTAGTAAAGGCAAGAGTCAAGGCC 1021
Db 1254 GGAACCAAGCAACCTTAAATGAAACCAAGAGGTTTCTAGTAAAGGCAAGAGTCAAGGCC 1313
QY 1022 TGCCCATCTCTCTGCTGCTTGATTAATGAAATCAAAAAAGAAATGATTCCTTTAATG 1081
Db 1314 TGCCCATCTCTCTGCTGCTTGATTAATGAAATCAAAAAAGAAATGATTCCTTTAATG 1373
QY 1082 GCCCAGTGTAGTATTAATACACATGCGAGAAATATCATTTATGTTACCCACAGAC 1141
Db 1374 GCCCAGTGTAGTATTAATACACATGCGAGAAATATCATTTATGTTACCCACAGAC 1433
QY 1142 AAAATTAATCTACACGGAATAAGGGTATGCCAAGGGGAAAGGCTCCTGGGGTAGACAAC 1201
Db 1434 AAAATTAATCTACACGGAATAAGGGTATGCCAAGGGGAAAGGCTCCTGGGGTAGACAAC 1493
QY 1202 CCATTCCACAGAGGTTTAGTTCCTGTAGAGGAGTACAGTAGTGTAGTCACTGACA 1261
Db 1494 CCATTCCACAGAGGTTTAGTTCCTGTAGAGGAGTACAGTAGTGTAGTCACTGACA 1553
QY 1262 GTGCGAGTTCAAGTGAAGCGATGCTGACTAGTCCACAGAGGTTTCCAGCGGGGTGACA 1321
Db 1554 GTGCGAGTTCAAGTGAAGCGATGCTGACTAGTCCACAGAGGTTTCCAGCGGGGTGACA 1613
QY 1322 GTCTGAAGACCTGCTACCTGTGAGTTGATGTAGAGAGAGCCCACTGA 1370
Db 1614 GTCTGAAGACCTGCTACCTGTGAGTTGATGTAGAGAGAGCCCACTGA 1662
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RESULT 6

US-10-311-840-2

; Sequence 2, Application US/10311840
; Publication No. US20030175808A1
; GENERAL INFORMATION:
; APPLICANT: KUROKAWA, Tomofumi
; APPLICANT: YAMADA, Takao
; APPLICANT: MORIMOTO, Shigeto

; TITLE OF INVENTION: No. US20030175808A1el Protein and its DNA
; FILE REFERENCE: 2738USOP
; CURRENT APPLICATION NUMBER: US/10/311,840
; PCT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: PCT/JP01/05263
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: JP 2000-191088
; PRIOR FILING DATE: 2000-06-21
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 2
; LENGTH: 1575
; TYPE: DNA
; ORGANISM: Human
; US-10-311-840-2

Query Match 77.9%; Score 1289; DB 12; Length 1575;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1289; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 2 TGAATAAAGATATAGTATCAGTAACAAGAGATATCTCAATGGCTCGAGGATGCAA 61
Db 287 TGAATAAAGATATAGTATCAGTAACAAGAGATATCTCAATGGCTCGAGGATGCAA 346
QY 62 TTTATCCTTAAGTCAACTGGGAATAAAGGGTTTCAGGATGAGATGATCTATCAGAAAC 121
Db 347 TTTATCCTTAAGTCAACTGGGAATAAAGGGTTTCAGGATGAGATGATCTATCAGAAAC 406
QY 122 TACATGACCAAGAAGATATGGCGAGCTCTCATCAGAAATAACATGCAACATATAATGG 181
Db 407 TACATGACCAAGAAGATATGGCGAGCTCTCATCAGAAATAACATGCAACATATAATGG 466
QY 182 GGCAGTGTCTGCGATTAAACTCTGGGGAAGAAACAAAGAGAACACACCTAGGAATG 241
Db 467 GGCAGTGTCTGCGATTAAACTCTGGGGAAGAAACAAAGAGAACACACCTAGGAATG 526
QY 242 TTCTAAACATAATCCCAGCAAGTATGAATATGCTAAAGCACACTCGAAGGATAAAAGA 301
Db 527 TTCTAAACATAATCCCAGCAAGTATGAATATGCTAAAGCACACTCGAAGGATAAAAGA 586
QY 302 AGCCTCAAGAGATTTCCAAAGCCAGAAAGTCCAGTAAAGAACAAAGACCCATCGTA 361
Db 587 AGCCTCAAGAGATTTCCAAAGCCAGAAAGTCCAGTAAAGAACAAAGACCCATCGTA 646
QY 362 TTCAACACACATGTACTACTTAAACATCTCTCAAAAGTCAAAATATCCCGTCAAT 421
Db 647 TTCAACACACATGTACTACTTAAACATCTCTCAAAAGTCAAAATATCCCGTCAAT 706
QY 422 TTCAAGGCGAGCGTTATACAGATCTTCAAGAGAGAGGGGACAATGATATATCTCCTTCA 481
Db 707 TTCAAGGCGAGCGTTATACAGATCTTCAAGAGAGAGGGGACAATGATATATCTCCTTCA 766
QY 482 GTGGGACGCGCAACCTTTTAAAGACATTTCTGTTAAAGAGAGAGCTTACTGTGCTGACC 541
Db 767 GTGGGACGCGCAACCTTTTAAAGACATTTCTGTTAAAGAGAGAGCTTACTGTGCTGACC 826
QY 542 TAGAAGCAAAAGATATTTCAACAGGGTTTTCAGGCCCAAGTGAAGCTGAGAGTACTCATC 601
Db 827 TAGAAGCAAAAGATATTTCAACAGGGTTTTCAGGCCCAAGTGAAGCTGAGAGTACTCATC 886
QY 602 TTGACACAAAAAAGCCAGGTTTATAATCAGATCCAGAGAGAGAGAAATGGTGGAAATA 661
Db 887 TTGACACAAAAAAGCCAGGTTTATAATCAGATCCAGAGAGAGAGAAATGGTGGAAATA 946
QY 662 CCATTGGAACCTAGGATGAAATGCGAAGAGGAGAGATGCTGTGATGTGAGCCTTTGAG 721
Db 947 CCATTGGAACCTAGGATGAAATGCGAAGAGGAGAGATGCTGTGATGTGAGCCTTTGAG 1006
QY 722 AGGCGACACGATATCATGGTAGTACCAATTTTAAAGGAGCTCCCTGGAGAGAGGAA 781
Db 1007 AGGCGACACGATATCATGGTAGTACCAATTTTAAAGGAGCTCCCTGGAGAGAGGAA 1066
QY 782 ACAGAGTGGATGCTGGCAGCCAAATGCTCAACAGGAGGTTGAGTTTCATTACCCCTC 841
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Db 1067 ACAGAGTGGATGCTGCGACGCCAAATAGTCTACCAAGGGAAGGTGAGTTTCATTACCCCTC 1126
QY 842 CTGCAACCTTCAAGAGAGAAAGAAAGAGGAGGAGTGTATGATGAGCTGAAAGTACCAACT 901
Db 1127 CTGCAACCTTCAAGAGAGAAAGAAAGAGGAGGAGTGTATGATGAGCTGAAAGTACCAACT 1186
QY 902 ATAATGAAATTCCTTAAATATGGCAAGGAGTACCAAGGAGGAGTGTATGATGAGCTGAAAT 961
Db 1187 ATAATGAAATTCCTTAAATATGGCAAGGAGTACCAAGGAGGAGTGTATGATGAGCTGAAAT 1246
QY 962 GGAACCAAGCAACCTTAAATATGAAAGAAAGGTTTCTAGTAAAGGCAAGGAGTGTAGGAGG 1021
Db 1247 GGAACCAAGCAACCTTAAATATGAAAGAAAGGTTTCTAGTAAAGGCAAGGAGTGTAGGAGG 1306
QY 1022 TGCCCATTCCTTCTGCTGCTGTGTAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATG 1081
Db 1307 TGCCCATTCCTTCTGCTGCTGTGTAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATG 1366
QY 1082 GCCCAGTCATGAGAAATATAATAACATGCGAGAAATATCATTTATGTACCCACAGAC 1141
Db 1367 GCCCAGTCATGAGAAATATAATAACATGCGAGAAATATCATTTATGTACCCACAGAC 1426
QY 1142 AAAATAATTCACAGGAATAAGGATGCGCAAGGGAAGGCTCTCGGGGTAGACAAC 1201
Db 1427 AAAATAATTCACAGGAATAAGGATGCGCAAGGGAAGGCTCTCGGGGTAGACAAC 1486
QY 1202 CCATTCACAGGAGGTTTGTTCCTGCTAGAGGATGACAGTGTAGTGTATCTGACA 1261
Db 1487 CCATTCACAGGAGGTTTGTTCCTGCTAGAGGATGACAGTGTAGTGTATCTGACA 1546
QY 1262 GTGGCAGTTCAAGTGAGAGCGATGTGTAC 1290
Db 1547 GTGGCAGTTCAAGTGAGAGCGATGTGTAC 1575

RESULT 7

US-09-794-422-1
; Sequence 1, Application US/09794422
; Publication No. US20030166239A1
; GENERAL INFORMATION:
; APPLICANT: Brown, Thomas A.
; APPLICANT: De Wet, Jeffrey R.
; APPLICANT: Gowen, Lori C.
; APPLICANT: Hames, Lynn M.
; TITLE OF INVENTION: Mammalian Osteoregulins
; FILE REFERENCE: PCL0445
; CURRENT APPLICATION NUMBER: US/09/794,422
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 60/185,617
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 60/234,500
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1655
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-09-794-422-1

Query Match 31.1%; Score 514.8; DB 12; Length 1655;
Best Local Similarity 63.0%; Pred. No. 1.8e-124;
Matches 994; Conservative 0; Mismatches 487; Indels 97; Gaps 9;

QY 58 TCAATTTTCTAAGTCACTGGGAATAAGGTTTGGAGTGGAGATGATGCTATCAGC 117
Db 170 TCTGTGAAGCTTGAGCCCATCTGGTGTAAAGGAACAGAGGGTGGCGGAGATGCTCCCTT 229
QY 118 AAATACATGACCAAGAAATATGGCGAGCTCTCATCAGAAATAAATCATCAATATA 177
Db 230 CACCTGCTTGACCAAGAACAGGAGGTTGCCACCTCTCTCAGAAATATCACTCAGCCTGTA 289
QY 178 ATGGGGCCAGTGACTGTGATTAACCTCTGGGGGAAGAAACAAAGAGAACACACCTAGG 237

Db 290 AAGAGTCTGTGACGGGAGTGAAGTACAGAGCGACAGAAACAAAGAGAAAGAAACCTCAG 349
QY 238 AATGTTCTAAACATATATCCAGCAAGTATGAATTTATGCTAAAGCACACACTCGAAGGATAAA 297
Db 350 AGTGTCTTAAGCGTAAATCCAAAGATGTCACAACTACTAAAGCTACTCAGAAGATACA 409
QY 298 AAGAGCCTCAAGAGATTTCCCAAGCCCAAGAAAGTCCAGTAAAGCAAGCAAGCACCCTAT 357
Db 410 GAGAACCAACAGAGGGATCTACTACTCCAGAACAGCCCAAGCAAGCAAGCAAGCACCCT 469
QY 358 CGTATTCAACACAAATTCAGTACTTAAACATCTCTCAAAAGTCAAAAGTCAAAAGTCAAAAGT 417
Db 470 CGGCCCCGAGAGACAGCAGTACCTTAACACATCTCCCCAAATCAGAAGATTTCTCAGT 529
QY 418 GATTTTGAAGGAGCGGTTTATACAGATCTTCAAGAGAGAGGGGACAAATGATATATCTCCT 477
Db 530 GACTTCGAGGACAGTGTCTTCCAGACCTTCTAGTGAGGGGGATTAATGATGTCCCTCCT 589
QY 478 TTCAAGTGGGAGCGCCCACTTTTAAAGACATTTCTGGTAAAGGAGAGTACTGTGCTCT 537
Db 590 TTCAAGTGGGAGTGGACCAATTTTATGACACTCTCCGACAGAGAGGTTCTGTGGATCT 649
QY 538 GACCTAGAGGCAAGATATTCAAACAGGTTTGCAGGCCCAAGTCAAGCTGAGAGTACT 597
Db 650 GATCTGAAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 706
QY 598 CATCTTGCACAAAAAGCCAGGTTTATATGAGATCTCCAGAGAGAGAGAAATGCTGGA 657
Db 707 GACCCACACACGATGAGTCTGAGTCTTATGAGATCTCCAGAGAGAGAGAGAGAGAGAGAG 766
QY 658 AATACATTTGAACTAGGATGAACTGCGAAGAGGAGAGATGCTGTTGATGTGAGCTT 717
Db 767 GGTGCTTATGCAACAG 826
QY 718 GTAGAGGCGAGCAACGATATCATGTAGTACCAATTTTAAAGGAGTCTCCCTGGAAGAG 777
Db 827 GTGAGAGGCGAGCAATGAAATCAGGGGAGTACCAATTTAGGGAGTCTCCCTGGAAGAG 886
QY 778 GGAACAGAGTGGATGCTGGCAGCCAAATGCTCACAGGGAAGGTTGAGTTTCAATTAC 837
Db 887 GGAACAGAGTGGATGCTGGCAGCCAAATGCTCACAGGGAAGGTTGAGTTTCAATTAC 946
QY 838 CTTCTGCAACCTTCAAG 897
Db 947 CCACAGGCGCTTCAAG 1006
QY 898 AACTATAATGAAATTCCTTAAATGCGAAGGAGTACCAAGAGAGAGAGAGAGAGAGAG 957
Db 1007 GGTTCATGAAATCCCAAG 1066
QY 958 AATAGGAACCAAGCAACCTTAAATGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1017
Db 1067 AAAGGAACCAAGTAACTTGTACTGAAAGCCAAAGTTCCCAAGGCAAGAGCAAGGCGAG 1126
QY 1018 GGCCTGCCCCCTTCTTCTGCTGCTGATGATGAAATCAAAAGTCAAAAGTCAAAAGTCA 1077
Db 1127 TCTTCTCAGAGTCTTGTGATGAGGTTAAAGTGAAGAGAGAGAGAGAGAGAGAGAGAG 1174
QY 1078 AATGCCCCAGTCTATGAGAAATATATACATGCGAAGAAATATCATTTATGTACCCAC 1137
Db 1175 AATAGTCTCAGTAG 1213
QY 1138 AGACAAATAATTTCTACCGGAATAAGGTTATGCGACAGGGAAGGCTCTCTGGG---GT 1194
Db 1214 AGAACAGCCACCTTACAGGATAGGGGATGTCACAGCGGAGAGGCTCTCTGGGCTCG 1273
QY 1195 AGACACCCCAATTCACAGAGAGGTTTATGTTCCCGTAGAGGATGACAGTAGTAGTCA 1254
Db 1274 AGAAGACCCCAATTCACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1330
QY 1255 TCTGACAGTGGCAGTTCAAGTGAGAGGATGGTGTAGTGTCCACAGAGAGTCCAGGG 1314

Db 1331 TCATCCAGTGGAGTTCTAGCGAGCAGTGGTGAAGTCTAGACCCCGGGTTGAACAGTT- 1389
Qy 1315 GGTGACAGTCTGAGACCTCGTACCTGTGAGTGTAGAGGAGACCACTGACAGC 1374
Db 1390 -----CCAGCTCT 1398
Qy 1375 TGACCAAGTGAAGAGAGATAGTGAAGAACTGAGTGAGCAGCAAGAAATCTGGTCTCCTT 1434
Db 1399 GGTCTGGAGAGAGAGGAGCGAGCAGGAGCTGAGCAAGGTACCACTGGTCACTC 1458
Qy 1435 GGGGGAATTTTGTCTATCTTAATAGTCACAGTAPAAAATCTATTAAGAGCTATAATGTT 1494
Db 1459 CA-GGACACTGTGCTGTTTGTAGTGGTTGTAATAAGAAATCCTACTCAAAGTTCTAATGCT 1517
Qy 1495 TTTAAGCAAAAAAATCATTACAGATCTATGAATAGTGAACATTTGAGTAGTGTGAT 1554
Db 1518 TTCTGAATAAAACCTTTGGAAGA-ATTATATAATAGGTAATATTTGACTAGCGGCC 1576
Qy 1555 TTAATAATAGTGGTGAATGTCAAAATGCTTC-TATGTTGTTTGTCTGTAGACATGA 1613
Db 1577 ATTAAAAATAGTCTGTGATGTCACAGGTGCTTGATATGATGATTTGCTCTTCAGACATGA 1636
Qy 1614 AATAAACAATATCTCTC 1631
Db 1637 AATAAAGAGGCTTTCTC 1654

RESULT 8

US-09-794-422-3
; Sequence 3, Application US/09794422
; Publication No. US20030166239A1
; GENERAL INFORMATION:
; APPLICANT: Brown, Thomas A.
; APPLICANT: De Wet, Jeffrey R.
; APPLICANT: Gowen, Lori C.
; APPLICANT: Hames, Lynn M.
; TITLE OF INVENTION: Mammalian Osteoregulins
; FILE REFERENCE: PC10445
; CURRENT APPLICATION NUMBER: US/09/794,422
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 60/185,617
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 60/234,500
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: Patent-In Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1682
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-794-422-3

Query Match 29.3%; Score 485.2; DB 12; Length 1682;
Best Local Similarity 62.3%; Pred. No. 1.1e-116;
Matches 1017; Conservative 0; Mismatches 483; Indels 132; Gaps 11;
Qy 16 AGTATCAGTAACAAGAGATACTCAATGGCTGAGGATGTCATTTATCTTAAGTCA 75
Db 166 AGCTGGGCAATCAAGACGATTCACAGGACTTGGCAGCATCTGTGATCTGATCCC 225
Qy 76 ACTGGGAATAAGGGTTTGGAGATGGAGATGCTATACGAAACTACATGACCAAGAA 135
Db 226 ACGGTGGATGAAGGCACAGAGGATGGCAAGGTGCTCTCTCCACCGCTGGCCAGGAC 285
Qy 136 GAATATGGCGCAGCTCTCATCAAAATACATCAACATATATATGGGCCAGTGAATGG 195
Db 286 AGTATGTTGCTGCTCCCTCTCAGAAATATACCGACGCTGTAAAGAGTCTAGTGA 345
Qy 196 ATTAAACTCTGGGGGAAGAAACAAAGAGAACACACCTAGGAAATGTTCTAAACAATC 255
Db 346 GCGGAACACTAGGAGGAAGAAACACAGGAGAGACCTCAGAGTGTCTTAGCGTAAT 405
Qy 256 CAGCAAGTATGATTAATGTTAAGCACACTCGAAGGATAAAGAAAGGCTCAAAGAGAT 315

Db 406 CCAGCAGATGTAATGATGCTAAAGTCTCTTAAAGACATAAAGAAATCAAGAGTTAT 465
Qy 316 TCCCAAGCCAGAAAAGTCCAGTAAAG-----CAAAGCACCCATCGTATTCAA 366
Db 466 CTGCTAACCCAGAGCAGCCCGTCAAAAGCAAAACACACACACCCGACACCGA 525
Qy 367 CACACATTTGACTACCTAAACATCTCTCAAAAGTCAAAAATCCCAAGTATTTGAA 426
Db 526 CGGAGCACTCACTACCTGACACATCTCCACAGATCAAGAGACTCCCAAGTATTTGAA 585
Qy 427 GGCAAGGTTATACAGATCTTCAAGAGAGAGGAGCAATATATATCTCTTCAAGTGG 486
Db 586 GGCAAGTGGTCCCAAGATCTTCTAGTGGGGAGATAATGATGTCCTCCCTTTTCAAGTGA 645
Qy 487 GACGGCCAACTTTTAAAGCACTTCTGTGTAAAGGAGAGCTACTGTCTCTGACTAGAA 546
Db 646 GATGGGCAACATTTTATGCACATTCCTGGCAAGG---AGTGTGGTCTGTGCTCTGAA 702
Qy 547 GGCAAGATATTCAAACAGGTTTGCAGGCCCAAGTGAAGCTGAGAGTACTCATCTTGAC 606
Db 703 AGCTCAACTAGTCGCC---CCTCTCAGGCTCCAGCAAGCTGAAGTTATTGACCCAT 759
Qy 607 AAAAAAGCCAGCTTATATAGATCCCAAGAGAGAGAAATGCTGGAATACCAT 666
Db 760 ATGATGGACTAGCTCTAATGAGATCCCGGGAGAGAGACATGTTGGCAGTGCCTAT 819
Qy 667 GGAAC TAGGGATGAACTGCGAAAGAGGAGAGATGCTGTTGATGTGACCTTTAGAGGGC 726
Db 820 GCAACAGAGACAAAGCTGCACAGGGGAGGCTCTGCAGTGGAGCCTTTGTTGGGGGC 879
Qy 727 AGCAACGATATCATGGTAGTACCAATTTTAAAGAGCTCCTCGAAGAGAGAAACAGA 786
Db 880 AGCAATGAATTCACAGGACACCAATTTTCAAGGAACTCCCGGAAAGAGGAAACAGA 939
Qy 787 GTGGATGCTGGCAGCCAAAATGCTCACAGGAGAGGTTTCAAGTTTCAATCCCTCCTGCA 846
Db 940 ATTAAATGCGGAGCCAAATGCTCATCAAGGAAAGTAGAATTTCACTATCCCAAGTG 999
Qy 847 CCTCAAAAGAGAAAAGAAAGGAGGAGTAGTGATGAGTCAAGTCAAGTCACTAAT 906
Db 1000 GCCTCGAGAGAAAGGTAAAGGGGGGCTGGAGCATGCA---GGAGAGCTGGTTACAAC 1056
Qy 907 GAAATCTTAAATGCGAAAGGAGTACCAAGAAAGGTTGATGATCATTTCAATAGAAC 966
Db 1057 GAAATCCCAAGAGCAGCAAGGTAGCTTAGCAAAAGATGCAGAGAGTCCAAAGGAAAC 1116
Qy 967 CAAGCAACCTTAAATGAAAAACAAAGGTTTCTAGTAAAGGCAAAAGTCAAGGCTGCC 1026
Db 1117 CAATTAACCTTGTCTGAGCCAAAGATTTCCAGGTAAGGCAAAAGCCAGGCGCTGCT 1176
Qy 1027 ATTCCTTCTGTTGCTTGTATATGAATCAAAAGCAAAATGATGATTCCTTTAATGGCCC 1086
Db 1177 CTGCCCTCTCACAGTCTTAGTAATGAGTTAAAGTGA----- 1214
Qy 1087 AGTCATGAGATATAATAACACATGCGCAAAATATCATTTATGTAACCCACAGACAAAT 1146
Db 1215 -----AGAAACCAATATGTTTCCATGACAAAAT 1245
Qy 1147 AATTTACACGGAATAAGGTTATGCCACAAGGAGAAAGGCTCCTGGGGT---AGACAACC 1203
Db 1246 AATCTTACCCGATTAAGAGGATGTCACAGCGAGAGGCTCCTGGCTTCGAGAAAGCC 1305
Qy 1204 CATTCACAGAGGTTTATGTTCCGTTAGAAGGATGACAGTAGTGAAGTCACTGACAGT 1263
Db 1306 AATTCACAGCGCGCTAGACCCGCCAAAG---AGACAGCAGCAGTCTGATCCAGT 1362
Qy 1264 GGCAGTTCAAGTGAGAGCGATGCTGATAGTCCACAGAGGTTCCAGCGGGGTGACAGT 1323
Db 1363 GGGAGTTCTAGTGAGAGTCACTGATAGTCCCTGGGATGAAACCAAGT----- 1411
Qy 1324 CTGAAGACCTCGTCACCTGTGAGTTGATGTAGAGGAGAGCCACCTGACAGTGAACAGGT 1383


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Query Match      2.8%; Score 46.8; DB 12; Length 345;
Best Local Similarity 46.8%; Pred. No. 0.068; 92; Indels 0; Gaps 0;
Matches 81; Conservative 0; Mismatches 92; Indels 0; Gaps 0;

QY 1483 GGCATAATGTTTTTAAGCAAAATAAATCATTACAGATCTATGAAATAGGTAACTTG 1542
DB 260 GGGNNTTTTTTTTTAAATAAATAAATAATTTTTTTTTTTTTTTTTTNNNNGGNN 201

QY 1543 AGTAGTGTCATTAAATAAGTTGGTAATGTCACAAATGCCCTTCTATGTTGTCCTC 1602
DB 200 NTNNNGNNGNTNNNAATAAATTTTTNNNNNTNNAANGNTTTNNNTTTTTTTTTNAGG 141

QY 1603 TGTAGACATCAAAATAACAAATCTCTCGATGATATAAATAAATAAATAAATAA 1655
DB 140 GGGGAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 88

RESULT 12
US-09-814-353-11753/c
; Sequence 11753, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11753
; LENGTH: 345
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 115, 144, 153, 155, 156, 157, 161, 163, 164, 167, 168, 170,
; LOCATION: 171, 172, 173, 179, 186, 187, 189, 190, 192, 194, 195, 196,
; LOCATION: 197, 200, 201, 202, 206, 207, 209, 211, 221, 256, 257, 265,
; LOCATION: 272, 273, 274, 276, 283, 287, 288, 290, 291, 293, 295
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 309, 314, 315, 327, 331, 332, 333
; OTHER INFORMATION: n = A,T,C or G
US-09-814-353-11753

Query Match      2.8%; Score 46.8; DB 12; Length 345;
Best Local Similarity 46.8%; Pred. No. 0.068; 92; Indels 0; Gaps 0;
Matches 81; Conservative 0; Mismatches 92; Indels 0; Gaps 0;

QY 1483 GGCATAATGTTTTTAAGCAAAATAAATCATTACAGATCTATGAAATAGGTAACTTG 1542
DB 260 GGGNNTTTTTTTTTAAATAAATAAATAATTTTTTTTTTTTTTTTTTNNNNGGNN 201

QY 1543 AGTAGTGTCATTAAATAAGTTGGTAATGTCACAAATGCCCTTCTATGTTGTCCTC 1602
DB 200 NTNNNGNNGNTNNNAATAAATTTTTNNNNNTNNAANGNTTTNNNTTTTTTTTTNAGG 141

QY 1603 TGTAGACATCAAAATAACAAATCTCTCGATGATATAAATAAATAAATAAATAA 1655
DB 140 GGGGAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 88

RESULT 14
US-09-887-576-831/c
; Sequence 831, Application US/09887576
; Patent No. US20020144047A1
; GENERAL INFORMATION:
; APPLICANT: Budworth, P.
; APPLICANT: Brown, D.
; APPLICANT: Chang, H.
; APPLICANT: Zhu, T.
; APPLICANT: Han, B.
; APPLICANT: Wang, X.
; APPLICANT: Cooper, Bret
; TITLE OF INVENTION: Promoters for regulation of plant expression
; FILE REFERENCE: 1360.001US1
; CURRENT APPLICATION NUMBER: US/09/887,576
; CURRENT FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: US 60/213,848
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/214,087
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/258,692
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 875
; SOFTWARE: FastSeq for Windows Version 4.0
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Db 200 NTNNNGNNGNTNNNAATAAATTTTTNNNNNTNNAANGNTTTNNNTTTTTTTTTNAGG 141
QY 1603 TGTAGACATCAAAATAACAAATCTCTCGATGATATAAATAAATAAATAAATAA 1655
DB 140 GGGGAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 88

RESULT 13
US-10-032-585-6930
; Sequence 6930, Application US/10032585
; Publication No. US20030180953A1
; GENERAL INFORMATION:
; APPLICANT: Terry, Roemer D.
; APPLICANT: Bo, Jiang
; APPLICANT: Charles, Boone
; APPLICANT: Howard, Bussey
; TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
; FILE REFERENCE: 10182-005-999
; CURRENT APPLICATION NUMBER: US/10/032,585
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 8000
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6930
; LENGTH: 2826
; TYPE: DNA
; ORGANISM: Candida albicans
US-10-032-585-6930

Query Match      2.8%; Score 46.6; DB 12; Length 2826;
Best Local Similarity 51.2%; Pred. No. 0.28;
Matches 109; Conservative 0; Mismatches 104; Indels 0; Gaps 0;

QY 951 TCATTCTAATAGGAACCAACCTTAATAATGAAAAACAAGGTTCTCTAGTAAGGCAA 1010
DB 21 TCCTAATAATAATAATAAATTCAGACATCAATCTCCACAGGGCTCTCTTCCAATAAGT 80
QY 1011 AAGTCAGGGCGCTGCCATTCTCTCGTGTCTTGTATGTAATGAAATCAAAACGAAATGA 1070
DB 81 AATATTGGCGATTCAATTTTGGTCTTGTATATGATGTTATTTAATGATAAACA 140
QY 1071 TTCCTTTAATGGCCCGATCATGAGAAATATAAACAATGCGAGAAAAATATCATTTGT 1130
DB 141 AACTCATATTAAACATACACCTTATATATACCAATATCTTGATPAAATCTCATGTGT 200
QY 1131 ACCCCACAGACAAAATAATTTCTACACGGATAA 1163
DB 201 AACCACTTTACAAAAATAATTTTACCACCAATAA 233
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RESULT 14
US-09-887-576-831/c
; Sequence 831, Application US/09887576
; Patent No. US20020144047A1
; GENERAL INFORMATION:
; APPLICANT: Budworth, P.
; APPLICANT: Brown, D.
; APPLICANT: Chang, H.
; APPLICANT: Zhu, T.
; APPLICANT: Han, B.
; APPLICANT: Wang, X.
; APPLICANT: Cooper, Bret
; TITLE OF INVENTION: Promoters for regulation of plant expression
; FILE REFERENCE: 1360.001US1
; CURRENT APPLICATION NUMBER: US/09/887,576
; CURRENT FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: US 60/213,848
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/214,087
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/258,692
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 875
; SOFTWARE: FastSeq for Windows Version 4.0
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; SEQ ID NO 831
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Oryza sativa
US-09-887-576-831

Query Match      2.8%; Score 45.8; DB 10; Length 2000;
Best Local Similarity 53.0%; Pred. No. 0.37;
Matches 98; Conservative 0; Mismatches 87; Indels 0; Gaps 0;

QY 1471 AATTCTATTAAAGCGTATAATGTTTTTAAGCAAAAAAATCATACAGATCTATGAAAT 1530
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Db 1269 ACTACTACTGCTGTATATACGTACTGTTACCAATACATATTACTCCATCTTATAAGA 1210

QY 1531 AGGTAACATTTGAGTAGGTCGTCATTTAAATAATAGTTGGTGAATGTCACAAATGCCCTTCTA 1590
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1209 AAGTAGTTTAGGCAATGCTTAAATCAAAATCTTAGGAATATAAATCATAAATAACITTTTA 1150

QY 1591 TGTGTTTTCGCTCTGTAGACATGAAATAAACAATATCTCTCGATGATAAAAAAATAAAA 1650
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1149 AGTTGTTGAGTTTGAAAATATAAAAAATTATATATAGATTTCCTTGAAAAATAATTT 1090

QY 1651 AAAAA 1655
    |||||
Db 1089 TATAA 1085

RESULT 15
US-10-312-841-2/c
; Sequence 2, Application US/10312841
; Publication No. US20030186277A1
; GENERAL INFORMATION:
; APPLICANT: Epigenomics AG
; TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des MHC
; FILE REFERENCE: E01/1208/WO
; CURRENT APPLICATION NUMBER: US/10/312,841
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 2
; LENGTH: 3673778
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; NAME/KEY: unsure
; LOCATION: (379615)
US-10-312-841-2

Query Match      2.7%; Score 44.8; DB 12; Length 3673778;
Best Local Similarity 50.5%; Pred. No. .70;
Matches 109; Conservative 0; Mismatches 107; Indels 0; Gaps 0;

QY 1440 AATTTTGGTATCTTAATAGTCACAGTATAAAATTCCTATTAAAGGCTATAATGTTTTTAA 1499
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1030117 ATCTTTTCATAAATTATAACAAATATACCACACTAATAATAAATATTAAATAACAAAA 1030058

QY 1500 GCAAAAAAATCATTCAGATCTATCAATAGTAGTACATTTGAGTAGGTCATTTAA 1559
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1030057 ATAAAAAATAAAAAAATAAATACTCTAAATTTTCCATTTTATTATTATA 1029998

QY 1560 AATAGTTGGTGAATGTCACAAATGCCTTCATGTTGCTCTGTAGACATGAAATAA 1619
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1029997 AATCTAAACTATCTCTTAAAAATAATATCTATTAAATTTTTTTTTTAAAAAATAAAC 1029938

QY 1620 ACAATATCTCTGATGATAAAAAAATAAAAAA 1655
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Db 1029937 ACTATACACTACTATAACATAAAAAAACTCTAAAAA 1029902
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OM protein - protein search, using sw model

Run on: November 26, 2003, 15:45:42 ; Search time 21 Seconds
(without alignments)
866.365 Million cell updates/sec

Title: US-09-700-696C-2

Perfect score: 2279

Sequence: 1 VNKEYSISNKENTHGLRMS.....RRDSSSESSDGSRRSDGD 430

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
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- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|---------------------|
| 1 | 140 | 6.1 | 772 | 1 | US-08-524-757-12 |
| 2 | 136 | 6.0 | 1187 | 1 | US-08-320-559-28 |
| 3 | 136 | 6.0 | 1187 | 3 | US-08-545-860D-28 |
| 4 | 136 | 6.0 | 1187 | 5 | PCT-US94-04496-28 |
| 5 | 136 | 6.0 | 1210 | 1 | US-08-320-559-26 |
| 6 | 136 | 6.0 | 1210 | 3 | US-08-545-860D-26 |
| 7 | 136 | 6.0 | 1210 | 5 | PCT-US94-04496-26 |
| 8 | 135.5 | 5.9 | 723 | 1 | US-07-814-964-11 |
| 9 | 135.5 | 5.9 | 723 | 1 | US-08-258-442-11 |
| 10 | 135.5 | 5.9 | 723 | 1 | US-08-328-809-6 |
| 11 | 135.5 | 5.9 | 723 | 4 | US-08-866-840-6 |
| 12 | 135.5 | 5.9 | 723 | 5 | PCT-US92-11107-11 |
| 13 | 134.5 | 5.9 | 1115 | 2 | US-08-568-459A-2 |
| 14 | 134.5 | 5.9 | 1115 | 2 | US-08-487-826B-2 |
| 15 | 134.5 | 5.9 | 1115 | 4 | US-09-210-288-2 |
| 16 | 134.5 | 5.9 | 1115 | 6 | 5198347-6 |
| 17 | 128 | 5.6 | 703 | 3 | US-08-910-925-4 |
| 18 | 127.5 | 5.6 | 1235 | 1 | US-08-118-101A-2 |
| 19 | 126.5 | 5.6 | 455 | 5 | PCT-US93-07261-13 |
| 20 | 126.5 | 5.6 | 1663 | 3 | PCT-US93-07261-16 |
| 21 | 125.5 | 5.5 | 1261 | 3 | US-09-208-742-4 |
| 22 | 125.5 | 5.5 | 1261 | 4 | US-09-332-295-2 |
| 23 | 125.5 | 5.5 | 1261 | 4 | US-09-709-979-2 |
| 24 | 124.5 | 5.5 | 1183 | 4 | US-08-134-001C-3530 |
| 25 | 123 | 5.4 | 493 | 3 | US-08-999-774A-12 |
| 26 | 123 | 5.4 | 1177 | 4 | US-09-134-001C-5106 |
| 27 | 123 | 5.4 | 1588 | 5 | PCT-US93-07261-11 |

| | | | | | | |
|----|-------|-----|------|---|---------------------|-------------------|
| 28 | 122 | 5.4 | 690 | 4 | US-09-134-001C-4568 | Sequence 4568, Ap |
| 29 | 121 | 5.3 | 1404 | 4 | US-08-801-308-1 | Sequence 1, Appli |
| 30 | 120.5 | 5.3 | 1435 | 2 | US-08-568-459A-4 | Sequence 4, Appli |
| 31 | 120.5 | 5.3 | 1435 | 2 | US-08-487-826B-4 | Sequence 4, Appli |
| 32 | 120.5 | 5.3 | 1435 | 4 | US-09-210-288-4 | Sequence 4, Appli |
| 33 | 120 | 5.3 | 1250 | 1 | US-08-441-139-9 | Sequence 9, Appli |
| 34 | 120 | 5.3 | 2842 | 1 | US-07-741-940-7 | Sequence 7, Appli |
| 35 | 120 | 5.3 | 2842 | 1 | US-08-289-548A-7 | Sequence 7, Appli |
| 36 | 120 | 5.3 | 2842 | 1 | US-08-452-654-7 | Sequence 7, Appli |
| 37 | 120 | 5.3 | 2842 | 4 | US-08-449-731-7 | Sequence 7, Appli |
| 38 | 120 | 5.3 | 2843 | 1 | US-07-741-940-2 | Sequence 2, Appli |
| 39 | 120 | 5.3 | 2843 | 1 | US-08-289-548A-2 | Sequence 2, Appli |
| 40 | 120 | 5.3 | 2843 | 1 | US-08-452-654-2 | Sequence 2, Appli |
| 41 | 120 | 5.3 | 2843 | 1 | US-08-452-655B-2 | Sequence 2, Appli |
| 42 | 120 | 5.3 | 2843 | 1 | US-08-452-655B-7 | Sequence 7, Appli |
| 43 | 120 | 5.3 | 2843 | 2 | US-08-370-235A-2 | Sequence 2, Appli |
| 44 | 120 | 5.3 | 2843 | 3 | US-08-450-582-2 | Sequence 2, Appli |
| 45 | 120 | 5.3 | 2843 | 3 | US-08-450-582-7 | Sequence 7, Appli |

ALIGNMENTS

RESULT 1

US-08-524-757-12
; Sequence 12, Application US/08524757
; Patent No. 5792634
; GENERAL INFORMATION:
; APPLICANT: Conaway, Ronald C.
; APPLICANT: Conaway, Joan W.
; APPLICANT: Bradsher, John N.
; TITLE OF INVENTION: RNA Polymerase Transcription Factor
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RICHARDS, MEDLOCK & ANDREWS
; STREET: 1201 Elm Street, Suite 4500
; CITY: Dallas
; STATE: TX
; COUNTRY: US
; ZIP: 75270-2197
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/524,757
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/13621
; FILING DATE: 29-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/160087
; FILING DATE: 30-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Harre, John A.
; REGISTRATION NUMBER: 37,345
; REFERENCE/DOCKET NUMBER: B35006CIPCIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (214) 939-4500
; TELEFAX: (214) 939-4600
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 772 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-524-757-12

Query Match 6.1%; Score 140; DB 1; Length 772;
Best Local Similarity 20.5%; Pred. No. 0.0014;
Matches 87; Conservative 49; Mismatches 144; Indels 144; Gaps 17;

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Qy 23 PKSTGNKGFEDGDAISKLHPOEYGAALINNNQHIMGPVTAIKLGEENKENTPRNVL 82
Db 210 PKGHSNAFQRLGASQERHLGEPHGKGVQNKHEH-----245
Qy 83 NIIPASMYAKAHSKDKKPPORDSOAKSPVKSKSTHRIQHNIIDYLKHLKSVKIPSPDFE 142
Db 246 -----KSSHKKRPVDAKDEKASVVSREKSH-----KALSK-----277
Qy 143 GSGYTDLOERGDNDISPSGSGQFPKDIIPGKGATGPDLEKGIQTGFPAGPSEAES-THL 201
Db 278 -----EENRRPPSGDNAREKP-PSSGVKKEKDREGSSLLKKCLPPSEASDNHL 325
Qy 202 DTGKPGYNEIPEREENGNTTGTDRDETAKEADADVSVLVEGSDIM-----GSTNFKEL 255
Db 326 -----KKPKHRD-PEKAK-----LDKSKQGLDSFDTG--KGAGDLLPKVKEKGSNNLKTP 372
Qy 256 PGREGRNVDAGSONAHQKV-----EFHYP-----PAPSKERKKEGSSDAES 298
Db 373 EGKVTNLDKSLGS-LPKVETDMEDEFEQPTMSFESYLSYDQPRKKKKIVKT-SATA 430
Qy 299 TNYNEIPKNGKSTRKGVHDHNRNQATLNEKQRPFSKGSQGL-----341
Db 431 LGDKGLKKNDSKSTGKNLDSVQKLPKVNKTKSEKAGADLAKLRKVPDVLPLPLPA 490
Qy 342 -----PIPSGLDNEIKNEMDSFNGPSHEN-----IITHGRKYHVHP-----378
Db 491 IQANYRPLPLLELISFQPKKAFSSPQEBEAGFTGRMNSKMGVYSGSKCAYLPKMMT 550
Qy 379 -HRQ 381
Db 551 LHQQ 554

RESULT 2
US-08-320-559-28
; Sequence 28, Application US/08320559
; Patent No. 5633135
; GENERAL INFORMATION:
; APPLICANT: Croce, Carlo
; APPLICANT: Canaani, Eli
; TITLE OF INVENTION: Diagnostics, Therapeutics and Methods for
; TITLE OF INVENTION: Detection and Treatment of Acute Leukemias
; TITLE OF INVENTION: Resulting from Chromosome Abnormalities in the
; TITLE OF INVENTION: All-1 Region
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5633135ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/320,559
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/062,443
; FILING DATE: 14 MAY 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/971,094
; FILING DATE: 30-OCT-92
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/888,830
; FILING DATE: 27-MAY-92
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/805,093
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; FILING DATE: 11-DEC-91
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-0855
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1187 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-320-559-28

Query Match 6.0%; Score 136; DB 1; Length 1187;
Best Local Similarity 20.6%; Pred. No. 0.0058;
Matches 86; Conservative 52; Mismatches 166; Indels 114; Gaps 14;

Qy 92 AKAHSKDKKKPQRDS-----QAQKSPVKSKSTHRIQHNIIDYLKHLKSVK 135
Db 530 SQEHSESKDPPKSSSKAPRAPPEAPHPGKESCKSPQAQEPPOQTGVTQPK-----K 584
Qy 136 KIPDFEGSGVTDLOERGDNDISPSGSGQFPKDIIP-----GKGE-----ATGPD 181
Db 585 PVKASARAGSRTSLQGEREPGLLPYGRSDQTSKDKPKVTKGRPRAAASNEPKPAVPPSS 644
Qy 182 EGKDIQTGFAGPSAES-----THLDTKPGY-----NEIPEREENGNTTGTDR 227
Db 645 EKKHKSLPAPSKALSGPEPAKONVEDRTEHFALVPLTSESQGPSPHSGSRTSGCQA 704
Qy 228 TAKEADADVSVLVEGSDNDIMGSTNFKELPGREGRNV-----DAGSONAHQKVE 276
Db 705 VVQEDSKRDLPLPLRDTKLLSPLRDTPPQSLMWKITLLLSRIPOPPGKGSQRKAE 764
Qy 277 FHYPPAPSKERKKEGSDAAESTYNEIPKNGKSTRKGVHDHNRNQATLNEKQRPFSKG 336
Db 765 DKQPPAGKHSSEKRSDDSS-----SKLAKRKGAEARDCD-----NKKIR-----805
Qy 337 KSQGLPIPSRGLDNEIKNEMDSFNGPSHENIIT-----HGRKYHVHPHQRNNSTRNK 388
Db 806 -----LEKEIKSQSSSSSSSHKESKTKPSPSSQSSSKKEMLPPIPPVSSSQKP 854
Qy 389 GMPQKGSG-----WGRQP-----HSNRRFSRRRRDDSSSDSGSSSE-----SDGD 430
Db 855 AKPALKSRREADTCGQDPPKSASTKSNHKDSIPKQRRVEGKRSRSSSEHKGSSGD 912

RESULT 3
US-08-545-860D-28
; Sequence 28, Application US/08545860D
; Patent No. 6040140
; GENERAL INFORMATION:
; APPLICANT: Croce, Carlo
; APPLICANT: Canaani, Eli
; TITLE OF INVENTION: Diagnostics, Therapeutics and Methods
; TITLE OF INVENTION: for Detection and Treatment of Acute Leukemias
; TITLE OF INVENTION: Resulting from Chromosome Abnormalities in the All-1 Region
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz &
; STREET: One Liberty Place, 46th floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08/545,860D
FILING DATE: 07-MAR-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/04496
FILING DATE: 22-APR-1994
PRIOR APPLICATION DATA: PCT/US92/10930
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/327,392
FILING DATE: 19-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/320,559
FILING DATE: 11-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/062,443
FILING DATE: 14-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/971,094
FILING DATE: 30-OCT-1992
PRIOR APPLICATION DATA: US 07/889,839
FILING DATE: 27-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/805,093
FILING DATE: 11-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Deluca Esq. Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-1262
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 1187 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-545-860D-28

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[illegible]

855 AKPALKRSREADTCGDDPKSASTSNHDKDSSIPKORRVEGKGRSSSEHKSSGD 912
 RESULT 4
 PCT-US94-04496-28
 ; Sequence 28, Application PC/TUS9404496
 ; GENERAL INFORMATION:
 ; APPLICANT: Croce, Carlo
 ; APPLICANT: Canaani, Eli
 ; TITLE OF INVENTION: Diagnostics, Therapeutics and Methods
 ; TITLE OF INVENTION: for Detection and Treatment of Acute Leukemias
 ; TITLE OF INVENTION: Resulting from Chromosome Abnormalities in the All-1
 ; NUMBER OF SEQUENCES: 86
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz &
 ; ADDRESSEE: Norris
 ; STREET: One Liberty Place, 46th floor
 ; CITY: Philadelphia
 ; STATE: Pennsylvania
 ; COUNTRY: USA
 ; ZIP: 19103
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US94/04496
 ; FILING DATE:
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: DeLuca Esq., Mark
 ; REGISTRATION NUMBER: 33,229
 ; REFERENCE/DOCKET NUMBER: TJU-1242
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (215) 568-3100
 ; TELEFAX: (215) 568-3439
 ; INFORMATION FOR SEQ ID NO: 28:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1187 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 PCT-US94-04496-28

| | | | | | |
|-----------------------|--------|--|--|-------------------|-----|
| Query Match | 6.0%; | Score 136; | DB 5; | Length 1187; | |
| Best Local Similarity | 20.6%; | Pred. No. 0.0058; | | | |
| Matches | 86; | Conservative 52; | Mismatches 166; | Indels 114; | |
| Gaps | 14; | | | | |
| QY | 92 | AKAHSKDKKPKQDS----- | QAQKSPVKSKSTHRIQHNIDYLKLSVKV | 135 | |
| Db | 530 | SQSHSGDKPPKSSSKAPPAPEAPHGKRSQKSPAQQEPPQRTVGTKPQK----- | K 584 | | |
| QY | 136 | KIPDFEGSGYTDQBERGDNDISPFGDGGQFFKDIP--KGKE----- | ATGPDFL | 181 | |
| Db | 585 | PVKASARAGSRTSLQGEREPGLLPYGSRDQTSKDQPKVTKGPRAAASNEPXPAPVPSS | 644 | | |
| QY | 182 | EGKDIQTGFAGPSEAS----- | THLDTKPGY----- | NRIPEEENGNTITGRDE | 227 |
| Db | 645 | EKKHKSSLPAPSKALSGPEAKNDVEDRTPHFALVPLTESQGPHGSGSRTSGCRQA | 704 | | |
| QY | 228 | TAKEADAIVSLVEGSDIMGSTNFKELPREGNRV----- | DAGSQNAHQKVE | 276 | |
| Db | 705 | VVVQESDKDRLLPLRDYTKLLSLPRDTPPPQSLMKITLILLSRIPQPPKSGSRQKAE | 764 | | |
| QY | 277 | FHYVPPAPSKERKKEGSDDAABESTNYNEIPKNGKSGSTRKGYDHSNRNQATLNEIKQRFPSKG | 336 | | |
| Db | 765 | DKQPPAGKXHSSEKSSDSS----- | SKLAKRKGEAERDC----- | NKKIR----- | 805 |
| QY | 337 | KSQGLPIPSRGLDNEIKNEMDSFNGSHENIIT----- | HGRKYHYVPHRONNSTRNK | 388 | |
| Db | 806 | ----- | LEKEIKSQSSSSSSHKSSSKTKPRPSQSSSKEMLPPLPPPVSSSSQKP | 854 | |


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; NAME: Deluca Esq., Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1262
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1210 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US94-04496-26

Query Match      6.0%; Score 136; DB 3; Length 1210;
Best Local Similarity 20.6%; Pred. No. 0.0059;
Matches 86; Conservative 52; Mismatches 166; Indels 114; Gaps 14;

QY 92 AKAHSDKKKKPQDSS-----QAQKSPVKSKSTHRIQHNIDYKLHLKSVK 135
Db 553 SQHSSSKDPPPKSSSKAPRAPEAPHGKRSCKSPAQOEPQRTVGTQKPK-----K 607
QY 136 KIPSPFEGGYTDLQERGNDISPPFGDQPPKIDP---GKGE-----ATGPD 181
Db 608 PVKASARAGSRTSLQGEREPGLPYGSRDQTSKDKPKVTKGRPRAAASNEPKPAVPPSS 667
QY 182 EGKDIQTQFAGPSEAB-----THLDTKKPGY-----NEIPEREENGNTIGTRDE 227
Db 668 EKKHKSSLPAPSKALSGPEPAKDNVEDTPEHFALVPLTESQGPSPHSGGRTSGCROA 727
QY 228 TAKEADADVSVLVEGNDIMGSTNFKELFREGNRV-----DAGSQNAHQKVE 276
Db 728 VVQEDSRKRLPLPLRDTKLLSPLRDTPPQSLMVKITLDDLRLSRIPQPPGKSGRQKAE 787
QY 277 FHPYPAPSKKEKESGSDAAESTNYNEIPKNGKSTRKGVDSNRNQATLNKQRPSPKG 336
Db 788 DKQPPAGKHSSEKSSDSS-----SKLAKRKGAEARDCD-----NKKIR----- 828
QY 337 KSQGLPIPSRLGDLNBIKNEIMDSFNGPSEHNIIT-----HGRKVYVYVPHRQNNSTRNK 388
Db 829 -----LEKIKQSSSSSSSHKESKTKSRPSSQSSKEMLPVPPVSSSSQKP 877
QY 389 GMPQKGS-----WGROP-----HSNRRFSSRRRDDSSSSDSSGSSSE---SDGD 430
Db 878 AKPALKRSRREADTCQDPPKPSASSTKSNHKDSIPKQRRVKGKSGRSSEHKGSSGD 935

RESULT 7
PCT-US94-04496-26
; Sequence 26, Application PC/TUS9404496
; GENERAL INFORMATION:
; APPLICANT: Croce, Carlo
; APPLICANT: Cavanaugh, Eli
; TITLE OF INVENTION: Diagnostics, Therapeutics and Methods
; TITLE OF INVENTION: for Detection and Treatment of Acute Leukemias
; TITLE OF INVENTION: Resulting from Chromosome Abnormalities in the All-1
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz &
; ADDRESSEE: Norris
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/04496
; FILING DATE:
```

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; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca Esq., Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1242
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1210 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US94-04496-26

Query Match      6.0%; Score 136; DB 5; Length 1210;
Best Local Similarity 20.6%; Pred. No. 0.0059;
Matches 86; Conservative 52; Mismatches 166; Indels 114; Gaps 14;

QY 92 AKAHSDKKKKPQDSS-----QAQKSPVKSKSTHRIQHNIDYKLHLKSVK 135
Db 553 SQHSSSKDPPPKSSSKAPRAPEAPHGKRSCKSPAQOEPQRTVGTQKPK-----K 607
QY 136 KIPSPFEGGYTDLQERGNDISPPFGDQPPKIDP---GKGE-----ATGPD 181
Db 608 PVKASARAGSRTSLQGEREPGLPYGSRDQTSKDKPKVTKGRPRAAASNEPKPAVPPSS 667
QY 182 EGKDIQTQFAGPSEAB-----THLDTKKPGY-----NEIPEREENGNTIGTRDE 227
Db 668 EKKHKSSLPAPSKALSGPEPAKDNVEDTPEHFALVPLTESQGPSPHSGGRTSGCROA 727
QY 228 TAKEADADVSVLVEGNDIMGSTNFKELFREGNRV-----DAGSQNAHQKVE 276
Db 728 VVQEDSRKRLPLPLRDTKLLSPLRDTPPQSLMVKITLDDLRLSRIPQPPGKSGRQKAE 787
QY 277 FHPYPAPSKKEKESGSDAAESTNYNEIPKNGKSTRKGVDSNRNQATLNKQRPSPKG 336
Db 788 DKQPPAGKHSSEKSSDSS-----SKLAKRKGAEARDCD-----NKKIR----- 828
QY 337 KSQGLPIPSRLGDLNBIKNEIMDSFNGPSEHNIIT-----HGRKVYVYVPHRQNNSTRNK 388
Db 829 -----LEKIKQSSSSSSSHKESKTKSRPSSQSSKEMLPVPPVSSSSQKP 877
QY 389 GMPQKGS-----WGROP-----HSNRRFSSRRRDDSSSSDSSGSSSE---SDGD 430
Db 878 AKPALKRSRREADTCQDPPKPSASSTKSNHKDSIPKQRRVKGKSGRSSEHKGSSGD 935

RESULT 8
US-07-814-964-11
; Sequence 11, Application US/07814964
; Patent No. 5359047
; GENERAL INFORMATION:
; APPLICANT: Donahue, Brian A.
; APPLICANT: Toney, Jeffrey H.
; APPLICANT: Bruhn, Suzanne L.
; APPLICANT: Pili, Pieter M.
; APPLICANT: Brown, Steven
; APPLICANT: Kellert, Patti
; APPLICANT: Essigmann, John M.
; APPLICANT: Lippard, Stephen J.
; TITLE OF INVENTION: DNA Structure Specific Recognition
; TITLE OF INVENTION: Protein and Uses Therefor
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: 2 Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/814,964
FILING DATE: 19911226
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/539,906
FILING DATE: 18-JUN-1990
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: MIT-4787AAA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 11
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 723 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Drosophila melanogaster
IMMEDIATE SOURCE:
CLONE: Drosophila SSRP (predicted)
FEATURE:
NAME/KEY: Domain
LOCATION: 458..507
OTHER INFORMATION: /label= Acidic
FEATURE:
NAME/KEY: Domain
LOCATION: 518..547
OTHER INFORMATION: /label= Basic I
FEATURE:
NAME/KEY: Domain
LOCATION: 547..620
OTHER INFORMATION: /label= HMG-box
FEATURE:
NAME/KEY: Domain
LOCATION: 632..649
OTHER INFORMATION: /label= Basic II
FEATURE:
NAME/KEY: Domain
LOCATION: 657..723
OTHER INFORMATION: /label= Mixed Charge
US-07-814-964-11

Query Match          5.9%; Score 135.5; DB 1; Length 723;
Best Local Similarity 23.2%; Pred.No.0.0032;
Matches      81; Conservative   37; Mismatches 114; Indels 117; Gaps    18;

QY       126 DYLK----HLSKVKKIPSDPEGGYTDLQBERGNDISPFSGDGFKXDI PG-KGEATCPD 180
           |||         :|||        :|||       :|||     :|||   :|||
Db       416 DYITQKLHVSNMK-----DKSYKYDV-DFGDS-----NENPDVLA RLKAEREKE 464

QY       181 LEGKDITGTAGPSEASTHLDTKKPGVNEIPEREENGNTIGTRDETAKEADVVS LV 240
           |||         :|||        :|||       :|||     :|||   :|||
Db       465 EDDDD-----GDSEESTEDF--KPNEESDVAEYDSNVESDSD---DSDASG---- 510

QY       241 EGSDNDIMGSTNFKE L PEGRNVDAGQN AHQGVEHYHPAPSKYEKRKG S----- 292
           |||         :|||        :|||       :|||     :|||   :|||
Db       511 -GGGDSGAKKKKKEKKEKKEKKKKKKKERTK-----KPSKKKKDGSKPKRATA F 562

QY       293 -----SDAAES-----TNYNEIPKNGKSTRGVDRSHNRNQATLNEKORPPSKGS QGL 341
           |||         :|||        :|||       :|||     :|||   :|||
Db       563 MLWLNDTFRESIKRENPGIKVTIAKKGEMWKELKDKSKWEDA AAKDKQRY----- 613

QY       342 PI PSRGLLDNLIKEMDSFGSPSHENITHGRKKHYIVPHQRNNSTRTNKMPGOKGSGWR-- 399
           |||         :|||        :|||       :|||     :|||   :|||

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; NAME/KEY: Domain
; LOCATION: 632..649
; OTHER INFORMATION: /label= Basic II
; FEATURE:
; NAME/KEY: Domain
; LOCATION: 657..723
; OTHER INFORMATION: /label= Mixed Charge
US-08-258-442-11

Query Match
Best Local Similarity 5.9%; Score 135.5; DB 1; Length 723;
Matches 81; Conservative 37; Mismatches 114; Indels 117; Gaps 18;

Qy 126 DYLK----HLKVKKIPSPFEGSGYTLQERGNDISPFSGDQGFDPG-KGEATGPD 180
Db 416 DYITQKHLVSNMCK-----DKSGYKDV-DFGSD-----NENEPDAYLARLKAAREKE 464
Qy 181 LEGKDITGTGAPGSEAEATHLDTKPGYNEIPREENGNTIGTRDETAKAADVSLV 240
Db 465 EDDDD-----GSDRESTDEDF-KPNEESDVAEEYDSNVESDSD--DSDASG--- 510
Qy 241 EGSNDIMGSTNFKELPQREGNRVDAQSNAHQKVEHYPPAPSKERKEGS----- 292
Db 511 -GGGSDGAKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK 562
Qy 293 ----SDAAES-----TNYNEIPKNGKSTRGVDSHNRNQATLNEKQRPFPKSGKSQL 341
Db 563 MLWINDTRESIKRENPGIKVTEIAKKGEMWKKELKDKSWEDAAAKDKQRY----- 613
Qy 342 PIPSRGLDNEIKNEMDSFNGPSHENIITHGRKHYVPHRQNNSTRNKGMPQKSGWGR-- 399
Db 614 -----HDEMRYKPEAGGSDSNEKG---GKSSKKRKT 642
Qy 400 QPHSNRR-----FSSRR--RDDSSESDSGSSSE-----SDGD 430
Db 643 EPSPKKANTSGSGFKSKEYISDDSTSDDEKDNPAKKKPPSPGD 691

RESULT 11
US-08-328-809-6
; Sequence 6, Application US/08328809
; Patent No. 5705334
; GENERAL INFORMATION:
; APPLICANT: Lippard, Stephen J.
; APPLICANT: Essigmann, John M.
; APPLICANT: Donahue, Brian A.
; APPLICANT: Toney, Jeffrey H.
; APPLICANT: Bruhn, Suzanne L.
; APPLICANT: Pil, Pieter M.
; APPLICANT: Brown, Steven
; APPLICANT: Kelletr, Patti
; TITLE OF INVENTION: Uses For DNA Structure-Specific
; TITLE OF INVENTION: Recognition Proteins
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Patent Administrator, Testa, Hurwitz & Thibault
; STREET: 53 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/328,809
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Fenton, Gillian M.
; REGISTRATION NUMBER: 36,508
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; OTHER INFORMATION: /label= Acidic
; FEATURE:
; NAME/KEY: Domain
; LOCATION: 518..547
; OTHER INFORMATION: /label= Basic I
; FEATURE:
; NAME/KEY: Domain
; LOCATION: 547..620
; OTHER INFORMATION: /label= HMG-box
; FEATURE:
; NAME/KEY: Domain
; LOCATION: 632..649
; OTHER INFORMATION: /label= Basic II
; FEATURE:
; NAME/KEY: Domain
; LOCATION: 657..723
; OTHER INFORMATION: /label= Mixed Charge
PCT-US92-11107-11

Query Match      5.9%; Score 135.5; DB 5; Length 723;
Best Local Similarity 23.2%; Pred. No. 0.0032;
Matches 81; Conservative 37; Mismatches 114; Indels 117; Gaps 18;

QY 126 DYLK-----HLKVKKPSDPFGSGYTLQERGNDISPFGSGGQPFKDIPG-KGEATGPD 180
Db 416 DYITQKLLHVSNMKG-----DKSGYKDV-DFGDS-----NENEPDAYLARLKAAREKE 464
QY 181 LEGKDQGTGAGSEABSTHLDTKKPGYNEIPEREENGNTIGTRDETAKEDADVSLV 240
Db 465 EDDDD-----GSDSESTDEDF-KPNESEDVAEYDSVSDSD-----DSDASG----- 510
QY 241 EGSNDIMGSTNFKELPREGNVDAGSQNAHQGVVEHYPPAPSKKKEKGS----- 292
Db 511 -GGGSDGAKKKKKEKKEKKEKKEKKEKKEK-----KSKKKKDGKPKRATTAF 562
QY 293 -----SAAES-----TNYNEIPKNGKSTRGVVHNSNQATLNEKQRFPSKGSQGL 341
Db 563 MLWLDNTRRESIKRENFGIKVTEIAKKGEMWKKELDKSKWEDAAAKDKQRY----- 613
QY 342 PIPSRGLDNEIKNEMDSFNGSPSHENIITHGRKYHYVPHRQNNNTRNKGMPQKGSWGR-- 399
Db 614 -----HDMRNYKPEAGGSDSDNFKG-----GKSKKRKT 642
QY 400 QPHSNR-----FSSRR--RDDSSSDSGSSSE-----SDGD 430
Db 643 EFSPPKANTSGSGFKSKYISDDTSSDDEKDNPEAKKSKPPSDGD 691

RESULT 13
US-08-568-459A-2
; Sequence 2, Application US/08568459A
; Patent No. 5849306
; GENERAL INFORMATION:
; APPLICANT: Sim, Kim L.
; APPLICANT: Chitnis, Chetan
; APPLICANT: Miller, Louis H.
; APPLICANT: Peterson, David S.
; APPLICANT: Su, Xin-zhaun
; APPLICANT: Wellens, Thomas E.
; TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
; TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSSEE: Knobbe Martens Olson & Bear
; CITY: Newport Beach
; STATE: California
; COUNTRY: US
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/568,459A
; FILING DATE: 07-DEC-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelisen, Ned
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: NIH121.001CP1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1115 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Plasmodium vivax
; US-08-568-459A-2

Query Match      5.9%; Score 134.5; DB 2; Length 1115;
Best Local Similarity 20.0%; Pred. No. 0.0071;
Matches 97; Conservative 80; Mismatches 220; Indels 89; Gaps 21;

QY 2 NKEYSISNKENTHGLRMSIYPKSTGNKGPEDGDADAIKSLHDOBEYGAALIRNMQHMG 61
Db 500 NKFISVKNKAEKVTAIVTFY-----DILKQ--ELDEFNEVAFENIKRDG 544
QY 62 PVTAILKLG-EENKENTPRNLNIIIPASMYAKAHKSKDKKKQPDQSOAKSPVKSKSTHR 120
Db 545 AYIELCVCSVEEAKKNTQEVVTVNDNAKSOA-TNSNPISQPVDSKAEKVP--GDSTH- 600
QY 121 IQHNIDYLKHLKSV-KKIPSPDFSGGYTDLQ-----ERCDNDISPFSGGQPFKDIPKGE- 175
Db 601 --GNVNSGQSSSTTGKAVTGDGQNGNQTPAESDVQRSDIAESVSAKNVDPQKSVSKRSD 658
QY 176 ---ATGPDLEGKDIQTGFAGPSEAEESTHLDTKKPG-----YNEI 211
Db 659 TASVTGIAEAGKE-NLGASNSRESEST-VEANSFGDDTVNSAIPVVGGENPLVTFYNGL 716
QY 212 PEREENGNN-----TIGTRDETAKEDADVSLVEGSDNDIMGSTNFKELPREGN 261
Db 717 RHKONSDDGPAESMANPDSNSKGETGKQDNDMAKATKDSNSSSDGTS-----SATGD 771
QY 262 RVDAGSQNAHQGVVEHYPPAPSKKKEKGS-----DAAESTNYNEIPKNGKST---RKG 315
Db 772 TTDADVREINKGVFEDRDKTVGSKDGGEDNSANKDAATVVGEDRIRENSAGGSTNDRSK 831
QY 316 VHSNRNQATLNEKQR--FPKSGKSOGLPIPSRG--LDNEIKNEMDSFNGSPSHENIITHG 371
Db 832 NDEKNGASTPDSKQSEDATALESLESTESGDRITNDTTNSLKNVKGKGDQKQHD 891
QY 372 RYHYVPHRQNNSTR-----NKGMPQKGSWGPQPHSNR-RFSSRRRDDSSSDSG 422
Db 892 FKSNDTPNEEPSNDQTTDAEGHDRDSIKNDKAE--RRKHMNKDTFTKNTNSHLNNSNNL 949
QY 423 SSSESD 428
Db 950 SNGKLD 955

RESULT 14
US-08-487-826B-2
; Sequence 2, Application US/08487826B
; Patent No. 5993827
; GENERAL INFORMATION:
; APPLICANT: Sim, Kim L.
; APPLICANT: Chitnis, Chetan
; APPLICANT: Miller, Louis H.
```

APPLICANT: Peterson, David S.
APPLICANT: Su, Xin-zhaun
APPLICANT: Wellem, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe Martens Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: California
COUNTRY: US
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,826B
FILING DATE: 10-SEP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Israel, Ned
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NIH121.001CP1
TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1115 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Plasmodium vivax
US-08-487-826B-2

Query Match 5.9%; Score 134.5; DB 2; Length 1115;
Best Local Similarity 20.0%; Pred. No. 0.0071;
Matches 97; Conservative 80; Mismatches 220; Indels 89; Gaps 21;

QY 2 NKEYSISNKTNGHGLRMSIYPSKTKNGKFGDGDGDAISKLHDOEYGAALIRNMQHIMG 61
Db 500 NKFIKVNAEKVQTAGIVTPY-----DILKQ--ELDEFNEVAFENEINKRDG 544

QY 62 PVTAKLLG-EENKENTPRVNLNIPASMYAKAHSKDKKKPQDSQAOKSPVKSSTHR 120
Db 545 AYELCVCSVEEAKKNTQEVVTVNDVNAKSAQA-TNSNPISQPVDSKAEKVP--GDSTH- 600

QY 121 IQHNIDYLKHLKSV-KKIPSDFGSGYTDLQ---ERGDNDISPFSGDGPFPKDPKGKE- 175
Db 601 --GNVNSGQDSSTTKGAVTGDGQNGTQPAESDVQSRDIAESVSAKNVDPQKSVKRSDD 658

QY 176 ---ATGPDLEKDIQITGFAGPSAEATHLDTKPKG-----YNEI 211
Db 659 TASVTGIAEAGKE-NLGASNSRPFEST-VEANSFGDDTVNSAIPVVSNGENPLVTPYNGL 716

QY 212 PEREENGNN-----TIGPRDETAKEADAVDSVLVEGSDNDIMGSTNFKELPGEGN 261
Db 717 RSKDMSDSDGPAESMANPDSNKGKGTGKQDNDMAKATKSSNSDGTG-----SATGD 771

QY 262 RVDAGSQNAHQGVFHYPPAPSKERKEGSS---DAAESTNYNEIPKNGKST---RKG 315
Db 772 TTDAVDREINKGVPEDRDKTVGSKDGGEDNSANKDAATVVGEDRIENSAGSTNDRSK 831

QY 316 VDSHNRQATLNKQR--FPKSKSQGLPIPSRG--LDNEIKNEMDSFNGPSHENIITHG 371
Db 832 NDTKNGASTPDSKQSEDATALSKTESLSTESGSDRTTNDTNSLENKNGGKEDLQKHD 891

QY 372 RKHYVPHRONNSTR-----NKGMPQKSGWGRPHSNR-RFSRRRDDSDSESDDSG 422
Db 892 FKSGNDTPNEEPNSDQTTDAEGHSDRDSIKNDKAE--RRKHWKDTFTKNTNSHLSNNNL 949

QY 423 SSSESDD 428
Db 950 SNGKLD 955

RESULT 15
US-09-210-288-2
Sequence 2, Application US/09210288
Patent No. 6392026
GENERAL INFORMATION:
APPLICANT: Sim, Kim L.
APPLICANT: Chitnis, Chetan
APPLICANT: Miller, Louis H.
APPLICANT: Peterson, David S.
APPLICANT: Su, Xin-zhaun
APPLICANT: Wellem, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe Martens Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: California
COUNTRY: US
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/210,288
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Fuller, Michael
REGISTRATION NUMBER: 36,516
REFERENCE/DOCKET NUMBER: NIH121.1FWDV1
TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1115 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Plasmodium vivax
US-09-210-288-2

Query Match 5.9%; Score 134.5; DB 4; Length 1115;
Best Local Similarity 20.0%; Pred. No. 0.0071;
Matches 97; Conservative 80; Mismatches 220; Indels 89; Gaps 21;

QY 2 NKEYSISNKTNGHGLRMSIYPSKTKNGKFGDGDGDAISKLHDOEYGAALIRNMQHIMG 61
Db 500 NKFIKVNAEKVQTAGIVTPY-----DILKQ--ELDEFNEVAFENEINKRDG 544

QY 62 PVTAKLLG-EENKENTPRVNLNIPASMYAKAHSKDKKKPQDSQAOKSPVKSSTHR 120
Db 545 AYELCVCSVEEAKKNTQEVVTVNDVNAKSAQA-TNSNPISQPVDSKAEKVP--GDSTH- 600

QY 121 IQHNIDYLKHLKSV-KKIPSDFGSGYTDLQ---ERGDNDISPFSGDGPFPKDPKGKE- 175
Db 601 --GNVNSGQDSSTTKGAVTGDGQNGTQPAESDVQSRDIAESVSAKNVDPQKSVKRSDD 658

| | | | | | |
|----|-----|-------|---|------------------------|-----|
| QY | 176 | --- | ATGPDLEKDIQTGFAGPSEASTHLDTKKPG----- | -----YNEI | 211 |
| Db | 659 | TA | SVTGIAAGRE-NLGASNPSEST-VEANSPGDDTVNSASIPVVG | ENPLVTPYNGL | 716 |
| QY | 212 | PERE | ENGGN-----TIGTRDETAKEADAVSVLVEGSNDIMG | STNFKELPGREGN | 261 |
| Db | 717 | RHSK | NSDSDGPAESMANPDSNSKGTGKGQDNDAKATKDS | SSSDGTS-----SATGD | 771 |
| QY | 262 | RVDAG | SONAHQKVEHYPPAPSKERKEGSS---DAESTNYNEIP | KNGKGST---RKG | 315 |
| Db | 772 | TTDA | VDRINKGVPEDRDKTVGSKDGGEDNSANKDAATVVG | EDRIRENSAGGSTNDRSK | 831 |
| QY | 316 | VDHS | NRNQATLNEKOR--FPSKKSQGLPIPSRG--LDNEI | KNEMDSFNGPSHENIITHG | 371 |
| Db | 832 | NOTE | KNGASTPDKQSEDATALSKESTESGDRTTNDT | NSLENKNGGKEKDLQKHD | 891 |
| QY | 372 | RKYH | YVPHRQNNSTR-----NKGMPQKGSWGQPHSNR-R | FSSRRRDDSSSSDSG | 422 |
| Db | 892 | FKS | NDTPNEEPNSDQTTDAEGHDRDSIKNDKAE--RR | KHMNKDTFTKNTNSHHLN>NNL | 949 |
| QY | 423 | SS | SED | 428 | |
| Db | 950 | SNG | KLD | 955 | |

Search completed: November 26, 2003, 15:49:09
Job time : 23 secs

Db 200 IQHNIDYLVKHLKSVKVKIPSPDFEGSGYTDLQERGDNDISPFSGDQPPKDIIPKGGEATGPD 259
Qy 181 LEGKDIQTGFAGPSEAEASTHLDTKKPGYNEIPEEREENGNTIGTRDETAKADAVDVSLV 240
Db 260 LEGKDIQTGFAGPSEAEASTHLDTKKPGYNEIPEEREENGNTIGTRDETAKADAVDVSLV 319
Qy 241 EGSNDIMGSTNFKELPGREGNRVDAGSQNAHQGVFHYPPAPSKKKEGSSDAAEASTN 300
Db 320 EGSNDIMGSTNFKELPGREGNRVDAGSQNAHQGVFHYPPAPSKKKEGSSDAAEASTN 379
Qy 301 YNEIPKNGKSTRKGVVPHRQNNSTRNKMPQKGSGWGRQPHSNRRFSSRRDDSSSD 360
Db 380 YNEIPKNGKSTRKGVVPHRQNNSTRNKMPQKGSGWGRQPHSNRRFSSRRDDSSSD 439
Qy 361 GPSHENIITHGRKYHYVPHRQNNSTRNKMPQKGSGWGRQPHSNRRFSSRRDDSSSD 420
Db 440 GPSHENIITHGRKYHYVPHRQNNSTRNKMPQKGSGWGRQPHSNRRFSSRRDDSSSD 499
Qy 421 SGSSSESDDG 430
Db 500 SGSSSESDDG 509

RESULT 2

US-09-794-422-6

; Sequence 6, Application US/09794422

; Publication No. US20030166239A1

; GENERAL INFORMATION:

; APPLICANT: Brown, Thomas A.

; APPLICANT: De Wet, Jeffrey R.

; APPLICANT: Gowen, Lori C.

; APPLICANT: Hames, Lynn M.

; TITLE OF INVENTION: Mammalian Osteoregulins

; FILE REFERENCE: PC10445

; CURRENT APPLICATION NUMBER: US/09/794,422

; CURRENT FILING DATE: 2001-02-27

; PRIOR FILING DATE: 60/185,617

; PRIOR FILING DATE: 2000-02-29

; PRIOR FILING DATE: 60/234,500

; PRIOR FILING DATE: 2000-09-22

; NUMBER OF SEQ ID NOS: 46

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 6

; LENGTH: 525

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-794-422-6

Query Match 99.9%; Score 2276; DB 12; Length 525;
Best Local Similarity 99.8%; Pred. No. 4.5e-173;
Matches 429; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VNKEYSISNKTNGHGLRMSIYPKSTGNKGFGDDAISKLHDQEEYGAALIRNMQHIM 60
Db 96 LNKEYSISNKTNGHGLRMSIYPKSTGNKGFGDDAISKLHDQEEYGAALIRNMQHIM 155
Qy 61 GPVTAIKLGEENKENTPRNVLNIIPASMYAKAHSKDKKKPQRDSQAQKSPVKSKSTHR 120
Db 156 GPVTAIKLGEENKENTPRNVLNIIPASMYAKAHSKDKKKPQRDSQAQKSPVKSKSTHR 215
Qy 121 IQHNIDYLVKHLKSVKVKIPSPDFEGSGYTDLQERGDNDISPFSGDQPPKDIIPKGGEATGPD 180
Db 216 IQHNIDYLVKHLKSVKVKIPSPDFEGSGYTDLQERGDNDISPFSGDQPPKDIIPKGGEATGPD 275
Qy 181 LEGKDIQTGFAGPSEAEASTHLDTKKPGYNEIPEEREENGNTIGTRDETAKADAVDVSLV 240
Db 276 LEGKDIQTGFAGPSEAEASTHLDTKKPGYNEIPEEREENGNTIGTRDETAKADAVDVSLV 335
Qy 241 EGSNDIMGSTNFKELPGREGNRVDAGSQNAHQGVFHYPPAPSKKKEGSSDAAEASTN 300
Db 336 EGSNDIMGSTNFKELPGREGNRVDAGSQNAHQGVFHYPPAPSKKKEGSSDAAEASTN 395

Qy 301 YNEIPKNGKSTRKGVVPHRQNNSTRNKMPQKGSGWGRQPHSNRRFSSRRDDSSSD 360
Db 396 YNEIPKNGKSTRKGVVPHRQNNSTRNKMPQKGSGWGRQPHSNRRFSSRRDDSSSD 455
Qy 361 GPSHENIITHGRKYHYVPHRQNNSTRNKMPQKGSGWGRQPHSNRRFSSRRDDSSSD 420
Db 456 GPSHENIITHGRKYHYVPHRQNNSTRNKMPQKGSGWGRQPHSNRRFSSRRDDSSSD 515
Qy 421 SGSSSESDDG 430
Db 516 SGSSSESDDG 525

RESULT 3

US-10-311-840-1

; Sequence 1, Application US/10311840

; Publication No. US20030175808A1

; GENERAL INFORMATION:

; APPLICANT: KUROKAWA, Tomofumi

; APPLICANT: YAMADA, Takao

; APPLICANT: MORIMOTO, Shigeto

; TITLE OF INVENTION: No. US20030175808A1el Protein and its DNA

; FILE REFERENCE: 2738USOP

; CURRENT APPLICATION NUMBER: US/10/311,840

; CURRENT FILING DATE: 2002-12-18

; PRIOR APPLICATION NUMBER: PCT/JP01/05263

; PRIOR FILING DATE: 2001-06-20

; PRIOR APPLICATION NUMBER: JP 2000-191088

; PRIOR FILING DATE: 2000-06-21

; NUMBER OF SEQ ID NOS: 10

; SEQ ID NO 1

; LENGTH: 525

; TYPE: PRT

; ORGANISM: Human

US-10-311-840-1

Query Match 99.9%; Score 2276; DB 12; Length 525;
Best Local Similarity 99.8%; Pred. No. 4.5e-173;
Matches 429; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VNKEYSISNKTNGHGLRMSIYPKSTGNKGFGDDAISKLHDQEEYGAALIRNMQHIM 60
Db 96 LNKEYSISNKTNGHGLRMSIYPKSTGNKGFGDDAISKLHDQEEYGAALIRNMQHIM 155
Qy 61 GPVTAIKLGEENKENTPRNVLNIIPASMYAKAHSKDKKKPQRDSQAQKSPVKSKSTHR 120
Db 156 GPVTAIKLGEENKENTPRNVLNIIPASMYAKAHSKDKKKPQRDSQAQKSPVKSKSTHR 215
Qy 121 IQHNIDYLVKHLKSVKVKIPSPDFEGSGYTDLQERGDNDISPFSGDQPPKDIIPKGGEATGPD 180
Db 216 IQHNIDYLVKHLKSVKVKIPSPDFEGSGYTDLQERGDNDISPFSGDQPPKDIIPKGGEATGPD 275
Qy 181 LEGKDIQTGFAGPSEAEASTHLDTKKPGYNEIPEEREENGNTIGTRDETAKADAVDVSLV 240
Db 276 LEGKDIQTGFAGPSEAEASTHLDTKKPGYNEIPEEREENGNTIGTRDETAKADAVDVSLV 335
Qy 241 EGSNDIMGSTNFKELPGREGNRVDAGSQNAHQGVFHYPPAPSKKKEGSSDAAEASTN 300
Db 336 EGSNDIMGSTNFKELPGREGNRVDAGSQNAHQGVFHYPPAPSKKKEGSSDAAEASTN 395
Qy 301 YNEIPKNGKSTRKGVVPHRQNNSTRNKMPQKGSGWGRQPHSNRRFSSRRDDSSSD 360
Db 396 YNEIPKNGKSTRKGVVPHRQNNSTRNKMPQKGSGWGRQPHSNRRFSSRRDDSSSD 455
Qy 361 GPSHENIITHGRKYHYVPHRQNNSTRNKMPQKGSGWGRQPHSNRRFSSRRDDSSSD 420
Db 456 GPSHENIITHGRKYHYVPHRQNNSTRNKMPQKGSGWGRQPHSNRRFSSRRDDSSSD 515
Qy 421 SGSSSESDDG 430
Db 516 SGSSSESDDG 525

RESULT 4

US-09-794-422-46
; Sequence 46, Application US/09794422
; Publication No. US20030166239A1
; GENERAL INFORMATION:
; APPLICANT: Brown, Thomas A.
; APPLICANT: De Wet, Jeffrey R.
; APPLICANT: Gowen, Lori C.
; APPLICANT: Hames, Lynn M.
; TITLE OF INVENTION: Mammalian Osteoregulins
; FILE REFERENCE: PC10445
; CURRENT APPLICATION NUMBER: US/09/794,422
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 60/185,617
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 60/234,500
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 46
; LENGTH: 540
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-794-422-46

Query Match 99.9%; Score 2276; DB 12; Length 540;
Best Local Similarity 99.8%; Pred. No. 4.7e-173;
Matches 429; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

| | | | |
|----|-----|--|-----|
| QY | 1 | VNKEYSISNKENTHNGLRMSIYPKSTGNKGFEGDDAISKLHQEYGAALIRNNQHIM | 60 |
| Db | 111 | LNKEYSISNKENTHNGLRMSIYPKSTGNKGFEGDDAISKLHQEYGAALIRNNQHIM | 170 |
| QY | 61 | GPVTAIKLGEENKENTPRNLNIIIPASMYAKAHSKDKKKPORDSQAQSPVKSKSTHR | 120 |
| Db | 171 | GPVTAIKLGEENKENTPRNLNIIIPASMYAKAHSKDKKKPORDSQAQSPVKSKSTHR | 230 |
| QY | 121 | IQHNIDYLKHLKSVKKIPSDFEGSGYTDLQERGNDISPFGDGQPKDIPGKEATGPD | 180 |
| Db | 231 | IQHNIDYLKHLKSVKKIPSDFEGSGYTDLQERGNDISPFGDGQPKDIPGKEATGPD | 290 |
| QY | 181 | LEGKDIQTGFAGPSEASTHLDTKPKGYNEIPREENGNTIGTRDETAKADAVDSL | 240 |
| Db | 291 | LEGKDIQTGFAGPSEASTHLDTKPKGYNEIPREENGNTIGTRDETAKADAVDSL | 350 |
| QY | 241 | EGSNDIMGSTNFKELPREGNRVDAGSNQAHQKVBFHYPPAPSKKKEGSSDAESTN | 300 |
| Db | 351 | EGSNDIMGSTNFKELPREGNRVDAGSNQAHQKVBFHYPPAPSKKKEGSSDAESTN | 410 |
| QY | 301 | YNEIPKNGKSTRKGVDSHNRNQTALNEKQRFPSKGSQGLPIPSRGLDNEIKNEMDSFN | 360 |
| Db | 411 | YNEIPKNGKSTRKGVDSHNRNQTALNEKQRFPSKGSQGLPIPSRGLDNEIKNEMDSFN | 470 |
| QY | 361 | GPSHENIITHGRKYHYVPHRQNNSTNKGMPQKGSWGRQPHSNRRFSSRRDDSSSSD | 420 |
| Db | 471 | GPSHENIITHGRKYHYVPHRQNNSTNKGMPQKGSWGRQPHSNRRFSSRRDDSSSSD | 530 |
| QY | 421 | SGSSSESDDG 430 | |
| Db | 531 | SGSSSESDDG 540 | |

RESULT 5

US-09-794-422-8
; Sequence 8, Application US/09794422
; Publication No. US20030166239A1
; GENERAL INFORMATION:
; APPLICANT: Brown, Thomas A.
; APPLICANT: De Wet, Jeffrey R.
; APPLICANT: Gowen, Lori C.
; APPLICANT: Hames, Lynn M.
; TITLE OF INVENTION: Mammalian Osteoregulins
; FILE REFERENCE: PC10445

US-09-794-422-8
; CURRENT APPLICATION NUMBER: US/09/794,422
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 60/185,617
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 60/234,500
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 556
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-794-422-8

Query Match 99.9%; Score 2276; DB 12; Length 556;
Best Local Similarity 99.8%; Pred. No. 4.9e-173;
Matches 429; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

| | | | |
|----|-----|--|-----|
| QY | 1 | VNKEYSISNKENTHNGLRMSIYPKSTGNKGFEGDDAISKLHQEYGAALIRNNQHIM | 60 |
| Db | 127 | LNKEYSISNKENTHNGLRMSIYPKSTGNKGFEGDDAISKLHQEYGAALIRNNQHIM | 186 |
| QY | 61 | GPVTAIKLGEENKENTPRNLNIIIPASMYAKAHSKDKKKPORDSQAQSPVKSKSTHR | 120 |
| Db | 187 | GPVTAIKLGEENKENTPRNLNIIIPASMYAKAHSKDKKKPORDSQAQSPVKSKSTHR | 246 |
| QY | 121 | IQHNIDYLKHLKSVKKIPSDFEGSGYTDLQERGNDISPFGDGQPKDIPGKEATGPD | 180 |
| Db | 247 | IQHNIDYLKHLKSVKKIPSDFEGSGYTDLQERGNDISPFGDGQPKDIPGKEATGPD | 306 |
| QY | 181 | LEGKDIQTGFAGPSEASTHLDTKPKGYNEIPREENGNTIGTRDETAKADAVDSL | 240 |
| Db | 307 | LEGKDIQTGFAGPSEASTHLDTKPKGYNEIPREENGNTIGTRDETAKADAVDSL | 366 |
| QY | 241 | EGSNDIMGSTNFKELPREGNRVDAGSNQAHQKVBFHYPPAPSKKKEGSSDAESTN | 300 |
| Db | 367 | EGSNDIMGSTNFKELPREGNRVDAGSNQAHQKVBFHYPPAPSKKKEGSSDAESTN | 426 |
| QY | 301 | YNEIPKNGKSTRKGVDSHNRNQTALNEKQRFPSKGSQGLPIPSRGLDNEIKNEMDSFN | 360 |
| Db | 427 | YNEIPKNGKSTRKGVDSHNRNQTALNEKQRFPSKGSQGLPIPSRGLDNEIKNEMDSFN | 486 |
| QY | 361 | GPSHENIITHGRKYHYVPHRQNNSTNKGMPQKGSWGRQPHSNRRFSSRRDDSSSSD | 420 |
| Db | 487 | GPSHENIITHGRKYHYVPHRQNNSTNKGMPQKGSWGRQPHSNRRFSSRRDDSSSSD | 546 |
| QY | 421 | SGSSSESDDG 430 | |
| Db | 547 | SGSSSESDDG 556 | |

RESULT 6

US-09-814-550-2
; Sequence 2, Application US/09814550
; Patent No. US20020102641A1
; GENERAL INFORMATION:
; APPLICANT: Schiavi, Susan
; APPLICANT: Madden, Stephen
; APPLICANT: Manavalan, Parthasarathy
; APPLICANT: Levine, Michael
; APPLICANT: Jan de Beur, Suzanne
; TITLE OF INVENTION: ONCOGENIC OSTEOBLAST-RELATED GENE 1
; FILE REFERENCE: 5014US
; CURRENT APPLICATION NUMBER: US/09/814,550
; CURRENT FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: US 60/191,786
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: US 60/241,598
; PRIOR FILING DATE: 2000-10-19
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 525

```
/ TYPE: PRT
; ORGANISM: Homo sapiens
US-09-814-550-2

Query Match          99.6%; Score 2269; DB 10; Length 525;
Best Local Similarity 99.5%; Pred. No. 1.6e-172;
Matches 428; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VNKEYSISNKNTHNGLRMSIYPKSTGNKGFEDGDDAISKLHDOBEYGAALIRNNMQHIM 60
Db LNKEYSISNKNTHNGLRMSIYPKSTGNKGFEDGDDAISKLHDOBEYGAALIRNNMQHIM 155

QY 61 GPVTAIKLGEENKENTPRNVLIIPASMYAKAHSKDKKKPQDSDQAOKSPVKSSTHR 120
Db GPVTAIKLGEENKENTPRNVLIIPASMYAKAHSKDKKKPQDSDQAOKSPVKSSTHR 215

QY 121 IQHNIDYLKHLKSVKVIIPSDFGSGYTDLOERGNNDISPFSGDQPPKDIPIGKGEATGPD 180
Db IQHNIDYLKHLKSVKVIIPSDFGSGYTDLOERGNNDISPFSGDQPPKDIPIGKGEATGPD 275

QY 216 IQHNIDYLKHLKSVKVIIPSDFGSGYTDLOERGNNDISPFSGDQPPKDIPIGKGEATGPD 240
Db IQHNIDYLKHLKSVKVIIPSDFGSGYTDLOERGNNDISPFSGDQPPKDIPIGKGEATGPD 335

QY 241 EGSNDIMGSTNFKELPGREGNRYDAGSONAHQGVKVEFHYPPAPSKKEKKGSSDAABSTN 300
Db EGSNDIMGSTNFKELPGREGNRYDAGSONAHQGVKVEFHYPPAPSKKEKKGSSDAABSTN 395

QY 301 YNEIPKNGKSTRKGVDSHNRNQTALNEKORFSPKSGKSGQLPIPSRGLDNEIKNEMDSFN 360
Db YNEIPKNGKSTRKGVDSHNRNQTALNEKORFSPKSGKSGQLPIPSRGLDNEIKNEMDSFN 455

QY 361 GPSHENIITHGRKYHYVPHRQNNSTRNKGMPQKGSGWGRQPHSNRRPSSRRDDSSSSD 420
Db GPSHENIITHGRKYHYVPHRQNNSTRNKGMPQKGSGWGRQPHSNRRPSSRRDDSSSSD 515

QY 421 SGSSSESDDG 430
Db SGSSSESDDG 525

RESULT 7
US-09-794-422-4
; Sequence 4, Application US/09794422
; Publication No. US20030186239A1
; GENERAL INFORMATION:
; APPLICANT: Brown, Thomas A.
; APPLICANT: De Wet, Jeffrey R.
; APPLICANT: Gowen, Lori C.
; APPLICANT: Hames, Lynn M.
; TITLE OF INVENTION: Mammalian Osteoregulins
; FILE REFERENCE: PC10445
; CURRENT APPLICATION NUMBER: US/09/794,422
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 60/185,617
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 60/234,500
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 441
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-794-422-4

Query Match          43.2%; Score 983.5; DB 12; Length 441;
Best Local Similarity 50.5%; Pred. No. 3.6e-70;
Matches 217; Conservative 52; Mismatches 134; Indels 27; Gaps 8;

QY 6 SISKENTHNGLRMSIYPKSTGNKGFEDGDDAISKLHDOBEYGAALIRNNMQHIMGPVTA 65
Db SCGNQDSIHKLDAASYVPDPTVDEGTGQGALLHPGQDRYGAALLRNITQPVKSLVTG 93

QY 66 IKLLGEENKENTPRNVLIIPASMYAKAHSKDKKKPQDSDQAOKSPVKS---KSTHRIQ 122
Db AELRREGNQEKRPQSVLSVIPADVNDKAVSLKDKKQESYLLLTQSSPVKSKHTKHTQTR 153

QY 123 HNIDYLKHLKSVKVIIPSDFGSGYTDLOERGNNDISPFSGDQPPKDIPIGKGEA-TPD 181
Db RSTHYLTHLPQIKKTPSDLEGGSPDLLVRGDNVDPFSGDQHFMHPIPKGGAGSGPE- 212

QY 182 EGKDIQTGAPGSEASTHLDTRKPGVNEIPEBEENGNTIGTRDETAKADADVDSLVE 241
Db --SSTRPISGSSKAEVIDPHMSGLSNEIPGREGHGSAYATRDKAQAGSAGGSLVG 270

QY 242 GSNIDIMGSTNFKELPGREGNRYDAGSONAHQGVKVEFHYPPAPSKKEKKGSSDAABSTN 301
Db GSNEITGSTNFKELPGREGNRYDAGSONAHQGVKVEFHYPPAPSKKEKKGSSDAABSTN 329

QY 302 NEIPKNGKSTRKGVDSHNRNQTALNEKORFSPKSGKSGQLPIPSRGLDNEIKNEMDSFN 361
Db NEIPKNGKSTRKGVDSHNRNQTALNEKORFSPKSGKSGQLPIPSRGLDNEIKNEMDSFN 383

QY 362 PSHENIITHGRKYHYVPHRQNNSTRNKGMPQKGSGW-GROPHSNRRPSSRRDDSSSSD 420
Db ---EN-----HYVHFGQNNLTPNKGMSORRGSWPSRRPNHRRASTQR-DSESSS 431

QY 421 SGSSSESDDG 430
Db SGSSSESDDG 441

RESULT 8
US-09-794-422-2
; Sequence 2, Application US/09794422
; Publication No. US20030186239A1
; GENERAL INFORMATION:
; APPLICANT: Brown, Thomas A.
; APPLICANT: De Wet, Jeffrey R.
; APPLICANT: Gowen, Lori C.
; APPLICANT: Hames, Lynn M.
; TITLE OF INVENTION: Mammalian Osteoregulins
; FILE REFERENCE: PC10445
; CURRENT APPLICATION NUMBER: US/09/794,422
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 60/185,617
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 60/234,500
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 435
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-794-422-2

Query Match          41.2%; Score 938.5; DB 12; Length 435;
Best Local Similarity 49.4%; Pred. No. 1.4e-66;
Matches 211; Conservative 45; Mismatches 146; Indels 25; Gaps 8;

QY 9 NKENTHNGLRMSIYPKSTGNKGFEDGDDAISKLHDOBEYGAALIRNNMQHIMGPVTAIKL 68
Db NQGNTH---LASVKPEPMVKGTGGGRDAPLHLLDQNRQATLLRNITQPVKSLVTGTEV 85

QY 69 LGEENKENTPRNVLIIPASMYAKAHSKDKKKPQDSDQAOKSPVKSSTHRIQHNDYL 128
Db QSDRNEKKKPPQSVLSVIPDVTNNTDYSEDTEQQRDLLONSPGQSKHTPRARRSTHYL 145

QY 129 KHLKSVKVIIPSDFGSGYTDLOERGNNDISPFSGDQPPKDIPIGKGEATGPDLE---GKD 185
Db THLPQIRKILSDFEDSASPDLLVRGDNVDPFSGDQHFMHPTDRGAVGSDPESSAGHP 205

QY 186 IQTGFAPGSEASTHLDTRKPGVNEIPEBEENGNTIGTRDETAKADADVDSLVEGSD 245
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Db 206 V----SGSSNVEIVDPHTNGLSGNEIPGREGHIGGAYATRGKTAQAGSADVSLVEGSNE 261
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Db 262 ITGSTKFLPELPGKGNRYVDASSQNAHQGVVEHYPPAPSKKKGSRHHTKAGYNEIP 321
QY 306 KNGKGSSTRKGVHDHNRNQATLNEKORFSPKSGKSQGLPIPSRGLDNEIKNEMDSFNGPSHE 365
Db 322 KSKKGASKDAEESKGNQVTLTESQRFPGKGGQS-----SHSLGNEVKSEEDSSNSLSRE 377
QY 366 NI-ITHGRKYHVPHRONNSTKNGMPQKGSW-GRQPHSNRRFSSRRDDSSSSSDGGS 423
Db 378 GIAIAHRRTSH-----PTRNRGMSQRSGSWARRPHPRRVSTRQR-DSSSSSSSGS 428
QY 424 SSESDDG 430
Db 429 SSESDDG 435

RESULT 9
US-09-812-485A-1
; Sequence 1, Application US/09812485A
; Publication No. US20020197267A1
; GENERAL INFORMATION:
; APPLICANT: Kumagai, Yoshinari
; APPLICANT: Blacher, Russel
; APPLICANT: Yoneda, Toshiyuki
; TITLE OF INVENTION: Integrin Binding Motif Containing
; TITLE OF INVENTION: Peptides and Methods of Treating Skeletal Diseases
; FILE REFERENCE: BEAR-006CIP
; CURRENT APPLICATION NUMBER: US/09/812,485A
; CURRENT FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 09/641,034
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptidic compound
US-09-812-485A-1

Query Match 22.6%; Score 514; DB 10; Length 97;
Best Local Similarity 100.0%; Pred. No. 1.2e-33;
Matches 97; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 105 DSQAKSPVKSKSTHRIQHNIDYKHLKSKVKKIPSDPFGSGYTDLQERGDNDISPFSGDG 164
Db 1 DSQAKSPVKSKSTHRIQHNIDYKHLKSKVKKIPSDPFGSGYTDLQERGDNDISPFSGDG 60

QY 165 QPFKDIQKGEATGDLGKDIQTGFAGPSEASTHL 201
Db 61 QPFKDIQKGEATGDLGKDIQTGFAGPSEASTHL 97

RESULT 10
US-09-812-485A-2
; Sequence 2, Application US/09812485A
; Publication No. US20020197267A1
; GENERAL INFORMATION:
; APPLICANT: Kumagai, Yoshinari
; APPLICANT: Blacher, Russel
; APPLICANT: Yoneda, Toshiyuki
; TITLE OF INVENTION: Integrin Binding Motif Containing
; TITLE OF INVENTION: Peptides and Methods of Treating Skeletal Diseases
; FILE REFERENCE: BEAR-006CIP
; CURRENT APPLICATION NUMBER: US/09/812,485A
; CURRENT FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 09/641,034
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 50

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptidic compound
US-09-812-485A-2

Query Match 10.3%; Score 235.5; DB 10; Length 47;
Best Local Similarity 94.0%; Pred. No. 7.3e-12;
Matches 47; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 105 DSQAKSPVKSKSTHRIQHNIDYKHLKSKVKKIPSDPFGSGYTDLQERGD 154
Db 1 DSQAKSPVKSKSTHRIQHNIDYKHLKSKVKKIPSDPFGSGYTD--RGD 47

RESULT 11
US-09-812-485A-4
; Sequence 4, Application US/09812485A
; Publication No. US20020197267A1
; GENERAL INFORMATION:
; APPLICANT: Kumagai, Yoshinari
; APPLICANT: Blacher, Russel
; APPLICANT: Yoneda, Toshiyuki
; TITLE OF INVENTION: Integrin Binding Motif Containing
; TITLE OF INVENTION: Peptides and Methods of Treating Skeletal Diseases
; FILE REFERENCE: BEAR-006CIP
; CURRENT APPLICATION NUMBER: US/09/812,485A
; CURRENT FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 09/641,034
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptidic compound
US-09-812-485A-4

Query Match 10.8%; Score 246; DB 10; Length 47;
Best Local Similarity 100.0%; Pred. No. 1.1e-12;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 108 AQKSPVKSKSTHRIQHNIDYKHLKSKVKKIPSDPFGSGYTDLQERGD 154
Db 1 AQKSPVKSKSTHRIQHNIDYKHLKSKVKKIPSDPFGSGYTDLQERGD 47

RESULT 12
US-09-812-485A-3
; Sequence 3, Application US/09812485A
; Publication No. US20020197267A1
; GENERAL INFORMATION:
; APPLICANT: Kumagai, Yoshinari
; APPLICANT: Blacher, Russel
; APPLICANT: Yoneda, Toshiyuki
; TITLE OF INVENTION: Integrin Binding Motif Containing
; TITLE OF INVENTION: Peptides and Methods of Treating Skeletal Diseases
; FILE REFERENCE: BEAR-006CIP
; CURRENT APPLICATION NUMBER: US/09/812,485A
; CURRENT FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 09/641,034
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Artificial Sequence
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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: November 29, 2003, 22:43:06 ; Search time 83 Seconds
(without alignments)
2286.684 Million cell updates/sec

Title: US-09-700-696C-2

Perfect score: 2279

Sequence: 1 VNKEYSISNKENHNGHRLMS.....RRDSSBSSDGGSSSDGD 430

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFWT=ptp -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA.*

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5: /cgn2_6/ptodata/1/ina/PCPUS COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| 1 | 150 | 6.6 | 6755 | 3 | US-08-931-999-4 |
| 2 | 140 | 6.1 | 2690 | 1 | US-08-524-757-11 |
| 3 | 138.5 | 6.1 | 2384 | 1 | US-07-814-964-10 |
| 4 | 138.5 | 6.1 | 2384 | 1 | US-08-258-442-10 |
| 5 | 138.5 | 6.1 | 2384 | 1 | US-08-328-809-5 |
| 6 | 138.5 | 6.1 | 2384 | 1 | US-08-866-840-5 |
| 7 | 138.5 | 6.1 | 2384 | 5 | PCT-US92-11107-10 |
| 8 | 137 | 6.0 | 9370 | 3 | US-08-320-559-27 |
| 9 | 137 | 6.0 | 9370 | 3 | US-08-545-860D-27 |
| 10 | 137 | 6.0 | 9370 | 5 | PCT-US94-04496-27 |
| 11 | 137 | 6.0 | 9391 | 1 | US-08-320-559-25 |
| 12 | 137 | 6.0 | 9391 | 3 | US-08-545-860D-25 |

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| 13 | 137 | 6.0 | 9391 | 5 | PCT-US94-04496-25 |
| 14 | 134.5 | 5.9 | 4084 | 2 | US-08-568-459A-1 |
| 15 | 134.5 | 5.9 | 4084 | 2 | US-08-487-826B-1 |
| 16 | 134.5 | 5.9 | 4084 | 4 | US-09-210-288-1 |
| 17 | 134.5 | 5.9 | 4084 | 6 | 5198347-5 |
| 18 | 129 | 5.7 | 3157 | 6 | 5198347-3 |
| 19 | 127.5 | 5.6 | 3707 | 1 | US-08-118-101A-1 |
| 20 | 127 | 5.6 | 2695 | 4 | US-09-706-197-3 |
| 21 | 127 | 5.6 | 4215 | 4 | US-09-620-312D-295 |
| 22 | 126.5 | 5.6 | 1393 | 5 | PCT-US93-07261-12 |
| 23 | 126.5 | 5.6 | 3773 | 3 | US-09-130-242-1 |
| 24 | 125.5 | 5.5 | 3825 | 3 | US-09-208-742-3 |
| 25 | 125.5 | 5.5 | 5173 | 4 | US-08-801-108-2 |
| 26 | 124.5 | 5.5 | 3552 | 4 | US-08-134-001C-693 |
| 27 | 123 | 5.4 | 1503 | 3 | US-08-999-774A-11 |
| 28 | 123 | 5.4 | 3534 | 4 | US-09-134-001C-2269 |
| 29 | 123 | 5.4 | 4766 | 5 | PCT-US93-07261-10 |
| 30 | 123 | 5.4 | 6775 | 4 | US-09-620-312D-289 |
| 31 | 122.5 | 5.4 | 3347 | 4 | US-09-702-705-318 |
| 32 | 122.5 | 5.4 | 3347 | 4 | US-09-736-457-318 |
| 33 | 122 | 5.4 | 2073 | 4 | US-09-134-001C-1731 |
| 34 | 122 | 5.4 | 43280 | 2 | US-08-804-227C-1 |
| 35 | 121 | 5.3 | 2004 | 1 | US-08-471-033-18 |
| 36 | 121 | 5.3 | 2004 | 2 | US-08-471-044-18 |
| 37 | 121 | 5.3 | 2004 | 2 | US-08-463-483A-18 |
| 38 | 121 | 5.3 | 2004 | 2 | US-08-471-046A-18 |
| 39 | 121 | 5.3 | 2004 | 2 | US-08-470-566B-18 |
| 40 | 121 | 5.3 | 2004 | 2 | US-08-469-334-18 |
| 41 | 121 | 5.3 | 2004 | 3 | US-09-300-529-18 |
| 42 | 121 | 5.3 | 2655 | 1 | US-08-471-033-17 |
| 43 | 121 | 5.3 | 2655 | 2 | US-08-471-044-17 |
| 44 | 121 | 5.3 | 2655 | 2 | US-08-463-483A-17 |
| 45 | 121 | 5.3 | 2655 | 2 | US-08-471-046A-17 |

c

ALIGNMENTS

RESULT 1

US-08-931-999-4
; Sequence 4, Application US/08931999
; Patent No. 6043219
; GENERAL INFORMATION:
; APPLICANT: Iandolo, John J.
; APPLICANT: Crupper, Scott S.
; TITLE OF INVENTION: Broad Spectrum Chemotherapeutic Peptide
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hovey, Williams, Timmons & Collins
; STREET: 2405 Grand Boulevard, Suite 400
; CITY: Kansas City
; STATE: Missouri
; COUNTRY: U.S.A.
; ZIP: 64108
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/931,999
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/710,561
; FILING DATE: 19-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Collins, John M.
; REGISTRATION NUMBER: 26,262
; REFERENCE/DOCKET NUMBER: 25043-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 816/474-9050
; TELEFAX: 816/474-9057
; INFORMATION FOR SEQ ID NO: 4:

COUNTRY: US
 ZIP: 75270-2197
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/524,757
 FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/13621

FILING DATE: 29-NOV-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/160087

FILING DATE: 30-NOV-1993

ATTORNEY/AGENT INFORMATION:

NAME: Harre, John A.

REGISTRATION NUMBER: 37,345

REFERENCE/DOCKET NUMBER: B35006CIPCIP

TELECOMMUNICATION INFORMATION:

TELEPHONE: (214) 939-4500

TELEFAX: (214) 939-4600

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 2690 base pairs

TYPE: nucleic acid

STRANDEDNESS: both

TOPOLOGY: both

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 33..2351

US-08-524-757-11

Alignment Scores:

Pred. No.: 0.00039 Length: 2690
 Score: 140.00 Matches: 87
 Percent Similarity: 32.08% Conservative: 49
 Best Local Similarity: 20.52% Mismatches: 144
 Query Match: 6.14% Indels: 144
 DB: 1 Gaps: 17

US-09-700-696c-2 (1-430) x US-08-524-757-11 (1-2690)

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 DB 660 CCTGGGAAGGCCACAGCAATGCTTTTCAGGACAGACTCGGGGCCAGCAAGACGAC 719
 QY 43 AspGlnGluGluTyrGlyAlaAlaLeuIleArgAsnAsnMetGlnHisIleMetGlyPro 62
 DB 720 CTGGTGACCCCATGGGAAGGGGTGTGAGTCACAAAGAGGACAC----- 767
 QY 63 ValThrAlaIleLysLeuGlyGluGluAsnLysGluAsnThrProArgAsnValLeu 82
 DB 767 ----- 767
 QY 83 AsnIleProAlaSerMetAsnTyrAlaLysAlaHisSerLysAspLysLysPro 102
 DB 768 -----AAATCTCCCAAGGACAAAGCAACGCCCGCTG 797
 QY 103 GlnArgAspSerGlnAlaGlnLysSerProValLysSerLysSerThrHisArgIleGln 122
 DB 798 GATGCCAGAGTGATGAGAGGGCTCTGTGTGAGCAGAGAGAAATCACAC----- 848
 QY 123 HisAsnIleAspTyrLeuLysHisLeuSerLysValLysLysIleProSerAspPheGlu 142
 DB 849 -----AAGGCCCTCTCCAA----- 863
 QY 143 GlySerGlyTyrThrAspLeuGlnGluArgGlyAspAsnAspLysSerProPheSerGly 162
 DB 864 -----GAGGAGAACCAGGACCCTCAGGG 890

QY 163 AspGlyGlnProPheLysAspIleProGlyLysGlyGluAlaThrGlyProAspLeuGlu 182
 DB 891 GACAATGCAGGGAGAAACCG---CCCTCTAGTCGCTAAAGAAAGACAGACAGAGAG 947
 QY 183 GlyLysAspIleGlnThrGlyPheAlaGlyProSerGluAlaGluSer---ThrHisLeu 201
 DB 948 GGCAGCAGCCTGAAGAGAAAGTGTTCCTCCCTCAGAGGCGCTTCAGAACACACCTG 1007
 QY 202 AspThrLysLysProGlyTyrAsnGluIleProGluArgGluGluAsnGlyGlyAsnThr 221
 DB 1008 -----AAAAAGCCAAAGCACAGAGAC---CCAGAGAAAGCCAAA----- 1043
 QY 222 IleGlyThrArgAspGluThrAlaLysGluAlaAspAlaValSerLeuValGlu 241
 DB 1044 -----TTGGACAAAAGCAAGAGTCTGGACAGCTTTCACACAGGA-----AAA 1088
 QY 242 GlySerAsnAspIleMet-----GlySerThrAsnPheLysGluLeu 255
 DB 1089 GGAGCAGGAGACCTGTTGCCCAAGTAAAGAGAGAGGTTCTAAACAACCTAAAGACTCCA 1148
 QY 256 ProGlyArgGluGlyAsnArgValAspAlaGlySerGlnAsnAlaHisGlnGlyLysVal 275
 DB 1149 GAGGGAAAGTCAAAACTAATTGGATAGAAAGTCACTGGGCTCC---CTCCCTAAAGTT 1205
 QY 276 -----GluPheHisTyrPro----- 280
 DB 1206 GAGGAGACAGATATGGAGATGAATTCGAGCAGCAACCATGTCTTTTGAATCTTACCTC 1265
 QY 281 -----ProAlaProSerLysGluLysArgLysGlySerSerAspAlaGluSer 298
 DB 1266 AGTATGACCAAGCCCGAAGAAAGAAAGAAAGTGTGAAAACCT---TCAGCCACGGCA 1322
 QY 299 ThrAsnTyrAsnGluIleProLysAsnGlyLysGlySerThrArgLysGlyValAspHis 318
 DB 1323 CTGGAGATAAAGGACTTAAAAAATGACTCTAAAGACACTGGTAAAAAAGCTTGACTCA 1382
 QY 319 SerAsnArgAsnGlnAlaThrLeuAsnGluLysGlnArgPheProSerLysGlyLysSer 338
 DB 1383 GTTCAGAAATATCCCAAGGTGACAAACCAAGTCAGAGAAGCGGCTGGAGCTGATTTA 1442
 QY 339 GlnGlyLeu----- 341
 DB 1443 GCCAAGCTGAGAAAGGTGCTGATGTGCTGAGTGTGCCAGACTTCCCGTTACCCGCG 1502
 QY 342 -----ProIleProSerArgGlyLeuAspAsnGluIleLysAsnGlu 355
 DB 1503 ATACAGGCCAATTACCGTCCACTGCTTCCTTCGAGCTGATATCTCTCTCCAGCCAAAG 1562
 QY 356 MetAspSerPheAsnGlyProSerHisGluAsn----- 366
 DB 1563 CGAAAAGCGTTCTCTTCACCCAGGAAGAAAGAGTGGATTTACTGGCGCAGAGATG 1622
 QY 367 -----IleIleThrHisGlyArgLysTyrHisTyrValPro----- 378
 DB 1623 AATCCAAAGATGAGGTGATTTCTGTTCCAAAGTGTGCTATCTCCCTAAAAATGATGACC 1682
 QY 379 ---HisArgGln 381
 DB 1683 TTGCACCAGCAA 1694

RESULT 3

US-07-814-964-10

; Sequence 10, Application US/07814964

; Patent No. 5359047

; GENERAL INFORMATION:

; APPLICANT: Donahue, Brian A.

; APPLICANT: Toney, Jeffrey H.

; APPLICANT: Bruhn, Suzanne L.

; APPLICANT: Pil, Pieter M.

; APPLICANT: Brown, Steven

; APPLICANT: Kellett, Patti

; APPLICANT: Essigmann, John M.

APPLICANT: Lipbard, Stephen J.
 TITLE OF INVENTION: DNA Structure Specific Recognition
 TITLE OF INVENTION: Protein and Uses Therefor
 NUMBER OF SEQUENCES: 13
 CORRESPONDENCE ADDRESS:
 ADDRESS: Hamilton, Brook, Smith & Reynolds, P.C.
 STREET: 2 Militia Drive
 CITY: Lexington
 STATE: MA
 COUNTRY: USA
 ZIP: 02173

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/814,964
 FILING DATE: 19911226

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/539,906

FILING DATE: 18-JUN-1990

ATTORNEY/AGENT INFORMATION:

NAME: Granahan, Patricia

REGISTRATION NUMBER: 32,227

REFERENCE/DOCKET NUMBER: MIT-4787AAA

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-861-6240

TELEFAX: 617-861-9540

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 2384 base pairs

TYPE: NUCLEIC ACID

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

ORGANISM: Drosophila melanogaster

IMMEDIATE SOURCE:

CLONE: Drosophila SSRP - composite sequence

POSITION IN GENOME:

CHROMOSOME/SEGMENT: 2

MAP POSITION: 60A 1-4

FEATURE:

NAME/KEY: CDS

LOCATION: 123..2291

US-07-814-964-10

Alignment Scores:

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|------------------------|----------|---------------|------|
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| Score: | 138.50 | Matches: | 99 |
| Percent Similarity: | 31.91% | Conservative: | 50 |
| Best Local Similarity: | 21.20% | Mismatches: | 136 |
| Query Match: | 6.08% | Indels: | 182 |
| DB: | 1 | Gaps: | 23 |

US-09-700-696C-2 (1-430) x US-07-814-964-10 (1-2384)

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| DB | 1187 | GGACGAGGATTCATCTATATCCACACCCGCTGCATATCGCTTTGAGGAG---- | 1241 |
| QY | 35 | pAspAlaIleSerLysLeuHisAspGlnGluTyrGlyAla----- | 49 |
| DB | 1242 | -----ATTAGTTCTGTGAACCTTGGCCGCGGCGGATCCACGGCGATCTTTGCGACTT | 1294 |
| QY | 50 | -----AlaLeuIleArgAsnAsnMetGlnHisIleMetGlyProValThrAlaIleLysLe | 68 |
| DB | 1295 | CGAAGTCACGCTCAAGAACGGAAGCTGTTACATCTTCTCTCCATC----- | 1340 |
| QY | 68 | uLeuGlyGluGlnLysGluAsnThrProArgAsnValLeuAsnIleIleProAlaSe | 88 |

| | | | |
|----|------|--|------|
| DB | 1341 | -----GAGAAGGAGGAG----- | 1352 |
| QY | 88 | rMetAsnTyrAlaLysAlaHisSerLysAspLysLysProGlnArgAspSerGlnAl | 108 |
| DB | 1353 | -----TATGCCAAGCTC----- | 1364 |
| QY | 108 | aGlnLysSerProValLysSerLysSerThrHisArgIleGlnHisAsnIleAspTyrIe | 128 |
| DB | 1365 | -----TTGCACTACAT | 1375 |
| QY | 128 | uLys-----HisLeuSerLysValLysIleProSerAspPheGluGlySe | 144 |
| DB | 1376 | CACACAGAAAGAGTTCATGTCAGCAATCGGCAAG-----GACAAGAG | 1420 |
| QY | 144 | rGlyTyrThrAspLeuGlnGluArgGlyAspAsnAspIleSerProPheSerGlyAspG1 | 164 |
| DB | 1421 | CGGCTACAAGGACGTG--GACTTTGGTGATTCGGAC-----AACGAGAA | 1462 |
| QY | 164 | yGlnProPheLysAspIleProGly---LysGlyGluAlaThrGlyProAspLeuGluG1 | 183 |
| DB | 1463 | CGAACCCAGATCCCTATCTGCTCGCTCAGGCTGAGCGGAGGAGGAGGAGGAGGAGGAG | 1522 |
| QY | 183 | yLysAspIleGlnThrGlyPheAlaGlyProSerGluAlaGluSerThrHisLeuAspTh | 203 |
| DB | 1523 | CGACGAT-----GGCGACTCGATGAGAGAGTCCACGATGAGGACTT | 1564 |
| QY | 203 | rLysLysProGlyTyrAsnGluIleProGluArgGluGluAsnGlyGlyAsnThrIleG1 | 223 |
| DB | 1565 | C--AAGCCCAACGAGAACGAGTCCGATGTCGCGGAGGAGTATGACACACGTCGAGAG | 1621 |
| QY | 223 | yThrArgAspGluThrAlaLysGluAlaAspAlaValAspValSerLeuValGluGlySe | 243 |
| DB | 1622 | TGATTCGAGCAT-----GACAGCGATGCTAGTGGC-----GGCGG | 1657 |
| QY | 243 | rAsnAspIleMetGlySerThrAsnPheLysGluLeuProGlyArgGluGlyAsnArgVa | 263 |
| DB | 1658 | AGGCGACACGCGCGCCCAAGAAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG | 1717 |
| QY | 263 | lAspAlaGlySerGlnAsnAlaHisGlnGlyLysValGluPheHisTyrProAlaApr | 283 |
| DB | 1718 | GGAGAAAAACACAGGAG | 1756 |
| QY | 283 | oSerLysGluLysArgLysGluGlySer-----AAACC | 1756 |
| DB | 1757 | CTCCAAG | 1816 |
| QY | 293 | ---SerAspAlaAlaGluSer-----ThrAsnTyrAsnGluI1 | 304 |
| DB | 1817 | GCTGACGACACGCGCGAGAGATCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG | 1876 |
| QY | 304 | eProLysAsnGlyLysGlySerThrArgLysGlyValAspHisSerAsnArgAsnGlnAl | 324 |
| DB | 1877 | CGCCAAAGAGGCGCGGAGATGTGGAAGAGAGCTGAAGACAAAGTCCAAGTGGAGGATGC | 1936 |
| QY | 324 | aThrLeuAsnGluLysGlnArgPheProSerLysGlyLysSerGlnGlyLeuProIlePr | 344 |
| DB | 1937 | GGCGGCCAAGGAGCAAGCGGCTAC----- | 1961 |
| QY | 344 | oSerArgGlyLeuAspAsnGluIleLysAsnGluMetAspSerPheAsnGlyProSerHi | 364 |
| DB | 1961 | ----- | 1961 |
| QY | 364 | sGluAsnIleIleThrHisGlyArgLysTyrHisTyrValProHisArgGlnAsnAsnSe | 384 |
| DB | 1962 | -----CACGACGAGATGCGCACTACACCTGACCGCGGCGGTGACAG | 2005 |
| QY | 384 | rThrArgAsnLysGlyMetProGlnGlyLysGlySerTrpGlyArg-----GlnProHi | 402 |
| DB | 2006 | CGCAACGAGAGAGGCT-----GGAAGTCTCTCAAGAGCGCAAGACGAGGAGCTTC | 2056 |
| QY | 402 | sSerAsnArgArg-----PheSerSerArgArg-----ArgAs | 413 |
| DB | 2057 | TCCATCAAGAGGCGAATACCTCGGCGAGCGGCTTCAAGAGCAAGAGGATACATTTCGGA | 2116 |

QY 413 pAspSerSerGluSerSerAspSerGlySerSerSerGlu----- 426
Db 2117 CGACGACTCCACGAGTCCCGACGAGGAGGACACAGGCTGCCAAGAGAGAGCAA 2176
QY 427 -----SerAspGlyAsp 430
Db 2177 GCCCCCATCCGACGCGCAT 2195

RESULT 4

US-08-258-442-10
; Sequence 10, Application US/08258442
; Patent No. 5670621
; GENERAL INFORMATION:
; APPLICANT: Donahue, Brian A.
; APPLICANT: Toney, Jeffrey H.
; APPLICANT: Bruhn, Suzanne L.
; APPLICANT: Pil, Pieter M.
; APPLICANT: Brown, Steven
; APPLICANT: Kellett, Patti
; APPLICANT: Essigmann, John M.
; APPLICANT: Lippard, Stephen J.
; TITLE OF INVENTION: DNA Structure Specific Recognition
; TITLE OF INVENTION: Protein and Uses Therefor
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: 2 Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/258,442
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/539,906
; FILING DATE: 18-JUN-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: MIT-4787AAA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2384 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Drosophila melanogaster
; IMMEDIATE SOURCE:
; CLONE: Drosophila SSRP - composite sequence
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: 2
; MAP POSITION: 60A 1-4
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 123...2291
US-08-258-442-10

Alignment Scores: 0.000459 Length: 2384
Pred. No.: 138.50 Matches:
Score:

Percent Similarity: 31.91% Conservative: 50
Best Local Similarity: 21.20% Mismatches: 136
Query Match: 6.08% Indels: 182
DB: 1 Gaps: 23
US-09-700-696C-2 (1-430) x US-08-258-442-10 (1-2384)
QY 16 GlyLeuArgMetSerIleTyrProLysSerThrGly-AsnLysGlyPheGluAspGlyAs 35
Db 1187 GGAGCGAGGATTCATCTATATCCAAAGCCACCCTGCATATCCGCTTTGAGGAG----- 1241
QY 35 pAspAlaIleSerLysLysLeuHisaspGlnGluGluTyrGlyAla----- 49
Db 1242 -----ATTAGTTCTGTGAACCTTCCCGCAGCGCGGATCCACGCGATCTTTCGACTT 1294
QY 50 ---AlaLeuIleArgAsnAsnMetGlnHisIleMetGlyProValThrAlaIleLysLe 68
Db 1295 CGAAGTGACGCTCAAGAACCGGACTGTTTCATCTTCTCTCCCATC----- 1340
QY 68 uLeuGlyGluGlnAsnLysGluAsnThrProArgAsnValLeuAsnIleleProAlaSe 88
Db 1341 -----GAGAAGGAGGAG----- 1352
QY 88 rMetAsnTyrAlaLysAlaHisSerLysAspLysLysLysProGlnArgAspSerGlnAl 108
Db 1353 -----TATGCCAAGCTC----- 1364
QY 108 aGlnLysSerProValLysSerLysSerThrHisArgIleGlnHisAsnIleAspTyrLe 128
Db 1365 -----TTCGACTACAT 1375
QY 128 uLys-----HisLeuSerLysValLysLysIleProSerAspGluGlySe 144
Db 1376 CACACAGAGAGAGTTGTCATGTGCAACATGGGCAAG-----GACAAGAG 1420
QY 144 rGlyTyrThrAspLeuGlnGlyArgGlyAspAsnAspIleSerProPheSerGlyAspGl 164
Db 1421 CGGCTACAGGACGTG---GACTTTGTGTGATTCGGAC-----AACGAGAA 1462
QY 164 yGlnProPheLysAspIleProGly---LysGlyGluAlaThrGlyProAspLeuGluGl 183
Db 1463 CGAACCCAGATGCTCTATCTGGCTCGCTCAAGGCTGAGCGAGGAGGAGGAGGAGAGA 1522
QY 183 yLysAspIleGlnThrGlyPheAlaGlyProSerGluAlaGluSerThrHisLeuAspTh 203
Db 1523 CGACGAT-----GGCGACTCGATGAAGAGTCCACGATGAGGACTT 1564
QY 203 rLysLysProGlyTyrAsnGluIleProGluArgGluGluAsnGlyGlyAsnThrIleGl 223
Db 1565 C---AAGCCACAGAGAACGATCCGATGTGCGCGAGGAGTATGACAGCACGTGGAGAG 1621
QY 223 yThrArgAspGluThrAlaLysGluAlaAspAlaValAspValSerLeuValGluGlySe 243
Db 1622 TGATTCGGACGAT-----GACAGCGATGCTAGTGGC-----GGCGG 1657
QY 243 rAsnAspIleMetGlySerThrAsnPheLysGluLeuProGlyArgGluGlyAsnArgVa 263
Db 1658 AGCGCAGACGCGAGCGGCGCAAGAAAAAGAGAGAGAAAGTCCGAGAGAAAGAGAAAAA 1717
QY 263 lAspAlaGlySerGlnAsnAlaHisGlnGlyLysValGluPheHisTyrProAlaPr 283
Db 1718 GGAGAAAAAACCAAGGAGAGAGACAAAG-----AAACC 1756
QY 283 oSerLysGluLysArgLysGluGlySer----- 292
Db 1757 CTCGAAGAGAGAGAGGACTCTGGCAACCCCAAGCGCGCCACCACCGCTTTCATGCTCTG 1816
QY 293 ---SerAspAlaAlaGluSer-----ThrAsnTyrAsnGluI 304
Db 1817 GCTGAACGACACGCGCGAGAGCATCAAGAGGAGGAAAAATCCGGCATAAAGTTTACCGAGAT 1876
QY 304 eProLysAsnGlyLysGlySerThrArgLysGlyValAspHisSerAsnArgAsnGlnAl 324
Db 304 eProLysAsnGlyLysGlySerThrArgLysGlyValAspHisSerAsnArgAsnGlnAl 324

Db 1877 GCCAAGAGCGCGCGAGATGCGAAGGAGCTGAGGACAACTCAAGTGGAGGATGC 1936
Qy 324 aThrLeuAsnGluLysGlnArgPheProSerLysGlyLysSerGlnGlyLeuProIlePr 344
Db 1937 GCGCGCCAAAGACAAAGACGCGCTAC----- 1961
Qy 344 oSerArgGlyLeuAspAsnGluIleLysAsnGluMetAspSerPheAsnGlyProSerHi 364
Db 1961 ----- 1961
Qy 364 sGluAsnIleIleThrHisGlyArgLysTyrHisTyrValProHisArgGlnAsnAsnSe 384
Db 1962 -----CACGACGAGATGCGCAACTACAAAGCTGAAGCGGCGGTGACAG 2005
Qy 384 rThrArgAsnLysGlyMetProGlnGlyLysGlySerTrpGlyArg-----GlnProHi 402
Db 2006 CGACAACGAGAAGGGT-----GGAAGTCTCCAAAGAGCGCAAGCGAGCGCTTC 2056
Qy 402 sSerAsnArgArg-----PheSerSerArgArg-----ArgAs 413
Db 2057 TCCATCCAAGAGCGGAATACCTCGGCGAGCGGCTTCAAGACGAAGGATACATTTCGGA 2116
Qy 413 pAspSerSerGluSerAspSerGlySerGlySerSerGlu----- 426
Db 2117 CGACGACTCCACACGCTCCGACGACGAGACAGCAACAGCGCTGCCAAGAAGAGAGCA 2176
Qy 427 -----SerAspGlyAsp 430
Db 2177 GCCCCCATTCGACGCGCAT 2195

RESULT 5

US-08-328-809-5
; Sequence 5, Application US/08328809
; Patent No. 5705334
; GENERAL INFORMATION:
; APPLICANT: Lippard, Stephen J.
; APPLICANT: Essigmann, John M.
; APPLICANT: Donahue, Brian A.
; APPLICANT: Toney, Jeffrey H.
; APPLICANT: Bruhn, Suzanne L.
; APPLICANT: Fil, Pieter M.
; APPLICANT: Brown, Steven
; APPLICANT: Kelleff, Patti
; TITLE OF INVENTION: Uses For DNA Structure-Specific
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patent Administrator, Testa, Hurwitz & Thibault
; STREET: 53 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/328,809
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Fenton, Gillian M.
; REGISTRATION NUMBER: 36,508
; REFERENCE/DOCKET NUMBER: MIT-023 (5473/24)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-248-7000
; TELEFAX: 617-248-7100
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2384 base pairs
; TYPE: nucleic acid

STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Drosophila melanogaster
IMMEDIATE SOURCE:
CLONE: Drosophila SSRP - composite sequence
POSITION IN GENOME:
CHROMOSOME/SEGMENT: 2
MAP POSITION: 60A 1-4
FEATURE:
NAME/KEY: CDS
LOCATION: 123..2291
US-08-328-809-5

Alignment Scores:
Pred. No.: 0.000459 Length: 2384
Score: 138.50 Matches: 99
Percent Similarity: 31.91% Conservative: 50
Best Local Similarity: 21.20% Mismatches: 136
Query Match: 6.08% Indels: 182
DB: 1 Gaps: 23

US-09-700-696C-2 (1-430) x US-08-328-809-5 (1-2384)

Qy 16 GlyLeuArgMetSerIleTyrProLysSerThrGly-AsnLysGlyPheGluAspGlyAs 35
Db 1187 GGAGCGAGGATTCATCTATATCCAAAGCCACCCTGCATATCCGCTTTGAGGAG---- 1241
Qy 35 pAspAlaIleSerLysLeuHisaspGlnGluGluTyrGlyAla----- 49
Db 1242 -----ATTAGTTCTGTGAACCTTGCCTCCGAGCGCGGATCCACGCGATCTTTCGACTT 1294
Qy 50 ---AlaLeuIleArgAsnAsnMetGlnHisIleMetGlyProValThrAlaIleLysLe 68
Db 1295 CGAAGTCAGCTCAAGAACCGAAGTGTTCATCTTCTCTCCATC----- 1340
Qy 68 uLeuGlyGluAsnLysGluAsnThrProArgAsnValLeuAsnIleIleProAlaSe 88
Db 1341 -----GAGAAGGAGGAG----- 1352
Qy 88 rMetAsnTyrAlaLysAlaHisSerLysAspLysLysLysProGlnArgaspSerGlnAl 108
Db 1353 -----TATGCCAAGCTC----- 1364
Qy 108 aGlnLysSerProValLysSerLysSerThrHisArgIleGlnHisAsnIleAspTyrLe 128
Db 1365 -----TTCGACTACAT 1375
Qy 128 uLys-----HisLeuSerLysValLysLysIleProSerAspPheGluGlySe 144
Db 1376 CACACAGAGAGAGTTGCTATGTCAGCAACATGGGCAAG-----GACAAGAG 1420
Qy 144 rGlyTyrThrAspLeuGlnIleArgGlyAspAsnAspIleSerProPheSerGlyAspGl 164
Db 1421 CGGCTACAGACGCTG-----GACTTTGGTGTATTCGGAC-----AACGAGAA 1462
Qy 164 yGlnProPheLysAspIleProGly---LysGlyGluAlaThrGlyProAspLeuGluI 183
Db 1463 CGAACCCAGATGCTCTGCTCGCTCAAGGCTGAGCGGAGGAGGAGGAGGACGA 1522
Qy 183 yLysAspIleGlnThrGlyPheAlaGlyProSerGluAlaGluSerThrHisLeuAspTh 203
Db 1523 CGACGAT-----GGCGACTCGGATGAAGAGTCCACCGATGAGGACTT 1564
Qy 203 rLysLysProGlyTyrAsnGluIleProGluArgGluGluAsnGlyGlyAsnThrIleGl 223
Db 1565 C---AAGCCCAACGAGACGAGTCCGATGTGCCGAGGAGTATGACAGCAACGCTGGAGAG 1621
Qy 223 yThrArgAspGluThrAlaLysGluAlaAspAlaValAspValSerLeuValGlyLys 243
Db 1622 TGATTCCGACGAT-----GACAGCGATGCTAGTGGC-----GCGCG 1657

1421 CGCTACAGGACGTG---GACTTTGGTGTATCGGAC-----AACGAGAA 1462
164 yGlnProPheLysAspIleProGly---LysGlyGluAlaThrGlyProAspLeuGluGl 183
1463 CGAACACAGATGCTATCTGCTCGCTCAAGTGTAGCGGAGGAGGAGGAGGAGGAGGAG 1522
183 yLysAspIleGlnThrGlyPheAlaGlyProSerGluAlaGluSerThrHisLeuAspTh 203
1523 CGACGAT-----GGCGACTCGGATGAAGATCCACCGATGAGGACTT 1564
203 rLysLysProGlyTyrrAsnGluLeuProGluArgGluGluAsnGlyGlyAsnThrIleGl 223
1565 C---AACCCACAGACGAGACGAGTCCGATGTGGCGGAGGAGTATGACAGCAACGTGGAGAG 1621
223 yThrArgAspGluThrAlaLysGluAlaAspAlaValAspValSerLeuValGluGlySe 243
1622 TGATTCGACGAT-----GACACGATGCTAGTGGC-----GGCGG 1657
243 rAsnAspIleMetGlySerThrAsnPheLysGluLeuProGlyArgGluGluAsnArgVa 263
1658 AGCGACAGACGACGCGCGCCAGAAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAA 1717
263 lAspAlaGlySerGlnAsnAlaHisGlnGlyLysValGluPheHisTyrrProAlaPr 283
1718 GGAGAAACACAG 1756
283 oSerLysGluLysArgLysGluGlySer----- 292
1757 CTCCAAG 1816
293 ---SerAspAlaAlaGluSer-----ThrAsnTyrrAsnGluI 304
1817 GCTGACGACAGCGCGGAT 1876
304 eProLysAsnGlyLysGlySerThrArgLysGlyValAspHisSerAsnArgAsnGlnAl 324
1877 CGCCAGAGAGAGCGCGGAG 1936
324 aThrLeuAsnGluLysGlnArgPheProSerLysGlySerGlnGlyLeuProIlePr 344
1937 GCGCGCCAG 1961
344 oSerArgGlyLeuAspAsnGluIleLysAsnGluMetAspSerPheAsnGlyProSerHi 364
1961 ----- 1961
364 sGluAsnIleIleThrHisGlyArgLysTyrrHisTyrrValProHisArgGlnAsnAsnSe 384
1962 -----CACGACGAGATGCGCAACTACAGAGCTGAAAGCTCAAGTCCAGTGGGAGGATGC 2005
384 rThrArgAsnLysGlyMetProGlnGlyLysGlySerTyrGlyArg-----GlnProHi 402
2006 CGACACAGAGAGGT-----GGAAAGTCTCTCAAGAGCGCAAGCGGAGGAGCTTC 2056
402 sSerAsnArgArg-----PheSerSerArgArg-----ArgAs 413
2057 TCCATCCAGAGAGCGGAGATACCTCGGCGAGCGGCTTCAAGAGCAAGGAGTACATTCGGA 2116
413 pAspSerSerGluSerSerAspSerGlySerSerGlySerSerGlu----- 426
2117 CGACGACTCCACCACTCGAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAA 2176
427 -----SerAspGlyAsp 430
2177 GCCCCCATCCGACGCGGAT 2195

RESULT 7
PCT-US92-11107-10
; Sequence 10, Application PC/TUS9211107
; GENERAL INFORMATION:
; APPLICANT: Donahue, Brian A.
; APPLICANT: Toney, Jeffrey H.
; APPLICANT: Bruhn, Suzanne L.

APPLICANT: Pil, Pieter M.
APPLICANT: Brown, Steven
APPLICANT: Kelllett, Patti
APPLICANT: Basigmann, John M.
APPLICANT: Lippard, Stephen J.
TITLE OF INVENTION: DNA Structure Specific Recognition
TITLE OF INVENTION: Protein and Uses Therefor
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESS: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: 2 Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/11107
FILING DATE: 19921218
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/539,906
FILING DATE: 18-JUN-1990
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: MIT-4787AAA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 2384 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
IMMEDIATE SOURCE:
ORGANISM: Drosophila melanogaster
CLONE: Drosophila SSRP - composite sequence
POSITION IN GENOME:
CHROMOSOME/SEGMENT: 2
MAP POSITION: 60A 1-4
FEATURE:
NAME/KEY: CDS
LOCATION: 123..2291
PCT-US92-11107-10
Alignment Scores:
Pred. No.: 0.000459 Length: 2384
Score: 138.50 Matches: 99
Percent Similarity: 31.91% Conservative: 50
Best Local Similarity: 21.20% Mismatches: 136
Query Match: 6.08% Indels: 182
DB: 5 Gaps: 23
US-09-700-696C-2 (1-430) x PCT-US92-11107-10 (1-2384)
QY 16 GlyLeuArgMetSerIleTyrrProLysSerThrGly-AsnLysGlyPheGluAspGlyAs 35
Db 1187 GGAGCGAGGATTCATCTATATCCACAGCCACGCGTCATATCCGCTTTGAGGAG----- 1241
QY 35 pAspAlaIleSerLysLeuHisAspGlnGluGluTyrrGlyAla----- 49
Db 1242 -----ATTAGTCTGTGAACTTTGCCCGCGAGCGCGGATCCACGCGATCTTCGACTT 1294
QY 50 ---AlaLeuIleArgAsnMetGlnHisIleMetGlyProValThrAlaIleLysLe 68

Db 1295 CGAAGTGCAGCTCAAGAACGGAACGTGTTCACATCTTCTCTCCATC----- 1340
Qy 68 uLeuGlyGluGluAsnLysGluAsnThrProArgAsnValLeuAsnIlelleProAlaSe 88
Db 1341 |||||-----GAGAAAGGAGGAG----- 1352
Qy 88 rMetAsnTyrAlaLysAlaHisSerLysAspLysLysProGlnArgAspSerGlnAl 108
Db 1353 |||||-----TATGCCAAGCTC----- 1364
Qy 108 acLlnLysSerProValLysSerLysSerThrHisArgIleGlnHisAsnIleAspTyrLe 128
Db 1365 |||||-----TTCGACTACAT 1375
Qy 128 uLys-----HisLeuSerLysValLysLysLysIleProSerAspPheGluGlySe 144
Db 1376 CACACAGAAAGATGTCATGTCAGCAACATGGGCAAG-----GACACAGAG 1420
Qy 144 rGlyTyrThrAspLeuGlnGluArgGlyAspAsnAspIleSerProPheSerGlyAspGl 164
Db 1421 |||||-----GACTTGGTGCATTCGGAC-----AACGAGAA 1462
Qy 164 yGlnProPheLysAspIleProGly---LysGlyGluAlaThrGlyProAspLeuGluGl 183
Db 1463 CGAACCATGCTATCTGGCTCGCTCAAGCTGAGCGGAGGAAAGGAGGAGACGA 1522
Qy 183 yLysAspIleGlnThrGlyPheAlaGlyProSerGluAlaGluSerThrHisLeuAspTh 203
Db 1523 CGACCAT-----GGCGACTCGGATGAAGATCCACGGATGAGGACTT 1564
Qy 203 rLysLysProGlyTyrAsnGluIleProGluArgGluGluAsnGlyGlyAsnThrIleGl 223
Db 1565 C---AAGCCCAACAGACGAGTCGATGTGGCCGAGGAGTATGACACACCGTGGAGAG 1621
Qy 223 yThrArgAspGluThrAlaLysGluAlaAspAlaValAspValSerLeuValGluGlySe 243
Db 1622 TCATTGGACGAT-----GACAGCGATGCTAGTGC-----GGCGG 1657
Qy 243 rAsnAspIleMetGlySerThrAsnPhelLysGluLeuProGlyArgGluGlyAsnArgVa 263
Db 1658 AGCGCACAGCGCGCGGCCCAAGAAAGAGAGGAAGTCCGAGAGAAAGAGAA 1717
Qy 263 lAspAlaGlySerGlnAsnAlaHisGlnGlyLysValGluPheHisTyrProProAlaPr 283
Db 1718 GGAGAAACACACAGGAGAGAGAGACAAAG-----AAACC 1756
Qy 283 oSerLysGluLysArgLysGluGlySer----- 292
Db 1757 TCCCAAGAAAGAGAGGACTCTGGCAACCCCAAGCGGCCACCGCTTTCATGCTCTG 1816
Qy 293 -----SerAspAlaIleGluSer-----ThrAsnTyrAsnGluIle 304
Db 1817 GGTGAACACACGCGCGAGAGATCAAGAGGGAATCCGGGCATAAAGGTTACCGAGAT 1876
Qy 304 eProLysAsnGlyLysGlySerThrArgLysGlyValAspHisSerAsnArgAsnGlnAl 324
Db 1877 GCCCAAGAGGCGCGAGATGTGGAAGGAGCTGAAGGACACAGTCCAAAGTGGAGGATGC 1936
Qy 324 aThrLeuAsnGluLysGlnArgPheProSerLysGlyLysSerGlnGlyLeuProIlePr 344
Db 1937 GCGCGCCCAAGGACACAGCGCGCTAC----- 1961
Qy 344 oSerArgGlyLeuAspAsnGluIleLysAsnGluMetAspSerPheAsnGlyProSerHi 364
Db 1961 ----- 1961
Qy 364 sGluAsnIleIleThrHisGlyArgLysTyrHisTyrValProHisArgGlnAsnAsnSe 384
Db 1962 -----CACGACGAGATGCGCAACTACAGCTGAAGCGGCGGTGACAG 2005
Qy 384 rThrArgAsnLysGlyMetProGluGlyLysGlySerTyrGlyArg-----GlnProHi 402
Db 2006 CGACACAGAGAGGGT-----GAAAGTCTCCAAAGAGCGGAGCGCTTC 2056

Qy 402 sSerAsnArgArg-----PheSerSerArgArg-----ArgAs 413
Db 2057 TCCATCCAAAGAGCGCAATACCTCGGGCAGCGCTTCAAGAGCAAGAGTACATTTCCGA 2116
Qy 413 pAspSerSerGluSerSerAspSerGlySerSerGlu----- 426
Db 2117 CGACGACTCCACGACTCCGAGCAGCAGAGAGACCAAGAGCTGCGCAAGAGAGCA 2176
Qy 427 -----SerAspGlyAsp 430
Db 2177 GCCCCCATCGACGCGCAT 2195
RESULT 8
US-08-320-559-27
Sequence 27, Application US/08320559
Patent No. 5633135
GENERAL INFORMATION:
APPLICANT: Croce, Carlo
APPLICANT: Canaan, Eli
TITLE OF INVENTION: Diagnostics, Therapeutics and Methods for
Detection and Treatment of Acute Leukemias
TITLE OF INVENTION: Resulting from Chromosome Abnormalities in the
TITLE OF INVENTION: All-1 Region
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5633135ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/320,559
FILING DATE:
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/08/062,443
FILING DATE: 14 MAY 1993
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/07/971,094
FILING DATE: 30-OCT-92
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/07/888,830
FILING DATE: 27-MAY-92
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/07/805,093
FILING DATE: 11-DEC-91
ATTORNEY/AGENT INFORMATION:
NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-0855
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 9370 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 469..4032
US-08-320-559-27
Alignment Scores:

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Pred. No.: 0.00499 Length: 9370
Score: 137.00 Matches: 100
Percent Similarity: 34.70% Conservative: 61
Best Local Similarity: 21.55% Mismatches: 192
Query Match: 6.01% Indels: 113
DB: 1 Gaps: 17

US-09-700-696C-2 (1-430) x US-08-320-559-27 (1-9370)

QY 37 AlalleSerLysLeuHisAspGlnGluTyrGlyAlaAlaLeuLeuAArgAsnMet 56
DB 1938 GCAGCTGACAACTGGCTGACCAAGTCCAGCAGCGCGCCGCGCCAGAGGGGCCAG 1997
QY 57 GlnHisIleMetGlyProValThrAlaIleLysLeuLeuGlyGluAluAsnLysGluAsn 76
DB 1998 GAGCAC---AGAGCCCCCAGCGCGCCAGCAGAGAGTAAAGGCGACGACGACGTCGCCAC 2054
QY 77 ThrProArgAsnValLeuAsn-----IleIleProAlaSerMetAsnTyrAlaLysAla 94
DB 2055 GAGTC-AGGACATTCGATCCAAAGATCTCTCCC-----CTAAAGCT 2098
QY 95 HisSerLysAspLysLysProGlnArg-----AspSerGlnAlaGln 109
DB 2099 CC-AGCAAGCCCCCGCGGCCCCAGCCGAGCCGCCAGCCCGGAGAAAGAGGAGTGTCCAG 2157
QY 110 LysSerProValLysSerLysThrHisArgIleGlnHisAsnIleAspTyrLeuLys 129
DB 2158 AAGTCTCGGCACAGCAGGAGCCGCCAAGAGGAAACCTGTGGAAACCAACACCCCAA 2217
QY 130 HisLeuSerLysValLysLysIleProSerAspPheGluGlySerGlyTyrThrAspLeu 149
DB 2218 -----AAACCTGTCAAGGCCTCTGCGCGGCGAGTTCACGACCCAGCGCTG 2262
QY 150 GlnGluArgGlyAspAsnAspIleSerProPheSerGlyAspGlyGlnProPheLysAsp 169
DB 2263 CAGGGGGAAGGAGGACAGCGGCTTCTTCCCTATGGCTCCCGAGACAGGACTTCCAAAGAC 2322
QY 170 IlePro-----GlyLysGlyGlu----- 175
DB 2323 AAGCCCAAGGTGAAGACGAAGAGCGCGCCCGCGCGCAGCAGCAAGCAACCAAGCCCA 2382
QY 176 AlaThrGlyProAspLeuGlyLysAspIleGlnThrGlyPheAlaGlyProSerGlu 195
DB 2383 GCAGTGCCTCCCTCCAGTGAGAGAAGAGCAGCAGAGCTCCCTCCCTGCGCCCTCTAAG 2442
QY 196 AlaGluSer-----ThrHisLeuAspThrLysLysProGlyTyr--- 208
DB 2443 GCTCTCTCAGCCCGCAGAACCCGCGAAGACAAATGTGGAGACAGGACCCCTGAGCACTTT 2502
QY 209 -----AsnGluIleProGluArgGluGluAsnGlyGlyAsnThr 221
DB 2503 GCTCTTGTCTCCCTGACTGAGAGCGAGCGGCCCCACACAGTGCAGCGCGCAGCAGACT 2562
QY 222 IleGlyThrArgAspGluThrAlaLysGluAlaAspAlaValAspValSerLeuValGlu 241
DB 2563 AGTGGTGCAGCGCAAGCGGTGTGGTCCAGGAGACAGCGCGCAAGAGCAGACTCCCATTTG 2622
QY 242 GlySerAsnAspIleMetGlySerThrAsnPheLysGluLeuProGlyArgGluGlyAsn 261
DB 2623 CCTTTGAGACACCAAGCTGCTCTCACCGCTCAGGAGCAGCTCTCCCGCACAAGAGTTG 2682
QY 262 ArgVal-----AspAlaGlySerGlnAsnAla 270
DB 2683 ATGCTGAAGATCAACCTAGACCTGCTCTCTCGGATACCCAGCTCCCGGAGGGGAGC 2742
QY 271 HisGlnGlyLysValGluPheHisTyrProProAlaProSerLysGluLysArgLysGlu 290
DB 2743 CGCAGAGGAAGAGCAGAAATAACAGCCCGCGCAGGAGGAAGAGCAGCTCTGAGAAG 2802
QY 291 GlySerSerAspAlaAlaGluSerThrAsnTyrAsnGluIleProLysAsnGlyLysGly 310
DB 2803 AGGAGCTCAGACACTCA-----AGCAAGTTGGCCAAAGAGAAAGGGT 2847
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QY 311 SerThrArgLysGlyValAspHisSerAsnArgAsnGlnAlaThrLeuAsnGluLysGln 330
DB 2848 GAAGCAGAAAGAGACTGTGAT-----AACAAAGAAATC 2880
QY 331 ArgPheProSerLysGlyLysSerGlnGlyLeuProIleProSerArgGlyLeuAspAsn 350
DB 2881 AGA-----CTGAGAG 2892
QY 351 GluIleLysAsnGluMetAspSerPheAsnGlyProSerHisGluAsnIleIleThr--- 369
DB 2893 GAAATCAATCACAGTCACTTCTTCATCTCTCCCAAGAAATCTTCTTAAACAAAG 2952
QY 370 -----HisGlyArgLysTyrHisTyrValProHisArgGlnAsn 382
DB 2953 CCCTCCAGCCCTCTCCACAGTCTCAAGAGGAAATGCTCCCGCCCGCCCGCTGCTCC 3012
QY 383 AsnSerThrArgAsnLysGlyMetProGlnGlyLysGlySer----- 396
DB 3013 TCGTCTCTCCAGAGCCAGCCAGCTTGAAGGTCAAGGTCAAGCGGGAGAGCAGACACC 3072
QY 397 TrpGlyArgGlnPro-----HisSerAsnArgArgPheSerSer 409
DB 3073 TGTGCCAGGAGCCCTCCCAAGAGTCCAGCAGTACCAAGAGCAACCAACAGACTCTTCC 3132
QY 410 ArgArgArgAspAspSerSerGluSerSerAspSerGlySerSerSerGlu----- 426
DB 3133 ATTCCCAAGCAGAGAGTAGAGGGGAGGGCTCCAGAGACTCTCTCGAGCACAAGGGT 3192
QY 427 SerAspGlyAsp 430
DB 3193 TCTTCCGAGAT 3204

RESULT 9
US-08-545-860D-27
; Sequence 27, Application US/08545860D
; Patent No. 6040140
; GENERAL INFORMATION:
; APPLICANT: Croce, Carlo
; APPLICANT: Canaan, Eli
; TITLE OF INVENTION: Diagnostics, Therapeutics and Methods
; TITLE OF INVENTION: for Detection and Treatment of Acute Leukemias
; TITLE OF INVENTION: Resulting from Chromosome Abnormalities in the All-1 Region
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz &
; ADDRESSEE: No. 6040140 is
; STREET: One Liberty Place, 46th floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/545,860D
; FILING DATE: 07-MAR-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/04496
; FILING DATE: 22-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/10930
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/327,392
; FILING DATE: 19-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/320,559
; FILING DATE: 11-OCT-1994
; PRIOR APPLICATION DATA:
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; APPLICATION NUMBER: US 08/062,443
; FILING DATE: 14-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/971,094
; FILING DATE: 30-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/888,839
; FILING DATE: 27-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/805,093
; FILING DATE: 11-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca Esq., Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1262
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9370 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 469..4032
US-08-545-860D-27

Alignment Scores:
Pred. No.: 0.00499 Length: 9370
Score: 137.00 Matches: 100
Percent Similarity: 34.70% Conservative: 61
Best Local Similarity: 21.55% Mismatches: 192
Query Match: 6.01% Indels: 113
Dbs: 3 Gaps: 17

US-09-700-696C-2 (1-430) x US-08-545-860D-27 (1-9370)
QY 37 AlaIleSerLysLeuHisAspGlnGluGluTyrGlyAlaAlaLeuIleArgAsnMet 56
Db 1938 GCAGCTGGACAACTGGCTGACCAAAAGTCAGCCAGCCAGCTGCCGCCACGAGGGCCCCAG 1997
QY 57 GlnHisIleMetGlyProValThrAlaIleLysLeuGluGluAsnLysGluAsn 76
Db 1998 GAGCAC---AGAGCCCCACCGCGGCACCCAGAGAGTAAAGGCAGCAGCAGTCCAC 2054
QY 77 ThrProArgAsnValLeuAsn-----IleIleProAlaSerMetAsnTyrAlaLysAla 94
Db 2055 GAGTC-AGGAGCATTTCTGAATCAAAAGATCTCTCCC-----CTAAAGCT 2098
QY 95 HisSerLysAspLysLysLysProGlnArg-----AspSerGlnAlaGln 109
Db 2099 CC-AGCAAGCCCCCGCGCCCCACCCGAAAGCCCCCAGCCGCGGAAAGAGGAGTGTCTAG 2157
QY 110 LysSerProValLysSerLysSerThrHisArgIleGlnHisAsnIleAspTyrLys 129
Db 2158 AAGTCTCGGCACAGCAGGAGGCCCCACAAAGGCAAAACCGTTTGGAAACCAACCAACCCAAA 2217
QY 130 HisLeuSerLysValLysLysIleProSerAspPheGluGlySerGlyTyrThrAspLeu 149
Db 2218 -----AAACCTGTCAAGGCTCTGCCCGGCGAGGTTTCAGGACCGCCGCTG 2262
QY 150 GlnGluArgGlyAspAsnAspIleSerProPheSerGlyAspGlnProPheLysAsp 169
Db 2263 CAGGGGGAAGGAGGACGAGGCTTCTTCTTATGGCTCCCGAGACCAGACTTCCAAAGAC 2322
QY 170 IlePro-----GlyLysGlyGlu----- 175
Db 2323 AAGCCCCAGGTGAAGACGAAAGAGCGGCCCGCGCGCGCAGCAAGCAACCAAGCCAGCCA 2382
QY 176 AlaThrGlyProAspLeuGluGlyLysAspIleGlnThrGlyPheAlaGlyProSerGlu 195

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Db 2383 GCAGTGCCCCCTCCAGTGAGAAGAAGACACAGAGTCCCTCCTGCCCCCTCTAAG 2442
QY 196 AlaGluSer-----ThrHisLeuAspThrLysLysProGlyTyr--- 208
Db 2443 GCTCTCTCAGGCCAGAACCCGGAAGGACAATGTGAGGACAGGACCCCTTGACACTTT 2502
QY 209 -----AsnGluIleProGluArgGluGluAsnGlyGlyAsnThr 221
Db 2503 GCTCTTTTCCCTGACTGAGAGCCAGGCCCCACCCACAGTGGCAGCGCAGCAGACT 2562
QY 222 IleGlyThrArgAspGluThrAlaLysGluAlaAspAlaValAspValSerLeuValGlu 241
Db 2563 AGTGGCTGCCCAAGCCGCTGGTGTCCAGGAGGACAGCGCGCAAGACAGACTCCCATTTG 2622
QY 242 GlySerAsnAspIleMetGlySerThrAsnPheLysGluLeuProGlyArgGluGlyAsn 261
Db 2623 CTTTTCAGAGACACCAAGCTGCTCTCACCGCTCAGGAGACACTCTCTCCCCACAAAGCTTG 2682
QY 262 ArgVal-----AspAlaGlySerGlnAsnAla 270
Db 2683 ATGCTGAAGATCACCTAGACCTGCTCTCTCGATATACCCAGCCTCCCGGAGGGGAGC 2742
QY 271 HisGlnGlyLysValGluPheHisTyrProAlaProSerLysGluLysArgLysGlu 290
Db 2743 CGCCAGAGAAAGCAGAGATAAACAGCCCGCCGAGGGAAGAACAGCTCTGTGAAG 2802
QY 291 GlySerSerAspAlaAlaGluSerThrAsnTyrAsnGluIleProLysAsnGlyLysGly 310
Db 2803 AGGAGCTCAGACAGCTCA-----AGCAAGTTGGCCAAAGAGAGAGGGT 2847
QY 311 SerThrArgLysGlyValAspHisSerAsnArgAsnGlnAlaThrLeuAsnGluLysGln 330
Db 2848 GAAGCAGAAAGAGACTGTGAT-----AACAGAAATC 2880
QY 331 ArgPheProSerLysGlySerGlnGlyLeuProIleProSerArgGlyLeuAspAsn 350
Db 2881 AGA-----CTGGAGAAG 2892
QY 351 GluIleLysAsnGluMetAspSerPheAsnGlyProSerHisGluAsnIleThr--- 369
Db 2893 GAATCAATCACAGTCATCTTCAITTCATCTCTCCACAAAGATCTTTAAACAAAG 2952
QY 370 -----HisGlyArgLysTyrHisTyrValProHisArgGlnAsn 382
Db 2953 CCCTCAGGCCCTCTCTCACAGTCTCTCAAGAGAAATGCTCCCCCGCCACCCGCTGCC 3012
QY 383 AsnSerThrArgAsnLysGlyMetProGlnGlyLysGlySer----- 396
Db 3013 TGTCTCTCCAGAGCCAGCCAGCTTCACTTAAGAGGTCAAGCGGGAAGCAGACACC 3072
QY 397 TrpGlyArgGlnPro-----HisSerAsnArgArgPheSerSer 409
Db 3073 TGTGCCAGGACCTCCCAAAAGTGCACAGTACCAGAGCAACCAAGACTCTTCC 3132
QY 410 ArgArgArgAspAspSerSerGluSerSerAspSerGlySerSerSerGlu----- 426
Db 3133 ATTCCCAAGCAGAGAAGTAGAGGGAAGGCTCCAGAAAGTCTCTCGGAGCAGCAGGCT 3192
QY 427 SerAspGlyAsp 430
Db 3193 TTTTCCGGAGAT 3204

RESULT 10
PCT-US94-04496-27
; Sequence 27, Application PC/TUS9404496
; GENERAL INFORMATION:
; APPLICANT: Croce, Carlo
; APPLICANT: Canaani, Eli
; TITLE OF INVENTION: Diagnostics, Therapeutics and Methods
; TITLE OF INVENTION: for Detection and Treatment of Acute Leukemias
; TITLE OF INVENTION: Resulting from Chromosome Abnormalities in the All-1
; NUMBER OF SEQUENCES: 86

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;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz &
;; ADDRESSEE: Norris
;; STREET: One Liberty Place, 46th floor
;; CITY: Philadelphia
;; STATE: Pennsylvania
;; COUNTRY: USA
;; ZIP: 19103
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US94/04496
;; FILING DATE:
;; CLASSIFICATION:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Deluca Esq., Mark
;; REGISTRATION NUMBER: 33,229
;; REFERENCE/DOCKET NUMBER: TJU-1242
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (215) 568-3100
;; TELEFAX: (215) 568-3439
;; INFORMATION FOR SEQ ID NO: 27:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 9370 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 469..4032
PCT-US94-04496-27

Alignment Scores:
Pred. No.: 0.00499 Length: 9370
Score: 137.00 Matches: 100
Percent Similarity: 34.70% Conservative: 61
Best Local Similarity: 21.55% Mismatches: 192
Query Match: 6.01% Indels: 113
DB: 17 Gaps: 17

US-09-700-696C-2 (1-430) x PCT-US94-04496-27 (1-9370)

QY 37 AlaIleSerLysLeuHisAspGlnGluTyrGlyAlaAlaLeuIleArgAsnMet 56
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DB 1938 GCAGCTGGACAACTGGCTGACCAAAAGTCAGCCAGCCAGCTGCCACAGAGGGCCCCAG 1997
QY 57 GlnHisIleMetGlyProValThrAlaIleLysLeuLeuGlyGluAlaAsnLysGluAsn 76
|||
|||
|||
DB 1998 GAGCAC---AGAGCCCCAGGGCCGCCAGAGAGTAAGGGCGAGCGACAGTGCAC 2054
QY 77 ThrProArgAsnValLeuAsn-----IleIleProAlaSerMetAsnTyrAlaLysAla 94
|||
|||
|||
DB 2055 GAGTC-AGGACATTCTGAATCAAAAGATCTCCCC-----CTAAAGCT 2098
QY 95 HisSerLysAspLysLysProGlnArg-----AspSerGlnAlaGln 109
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DB 2099 CC-AGCAAGCCCCCGGGCCCCACCCGGAAGCCCCCAGCCCGGGAAGAGAGTGTCCAG 2157
QY 110 LysSerProValLysLysSerThrHisArgIleGlnHisAsnIleAspTyrLeuLys 129
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DB 2158 AAGTCTCCGGCAGCAGCAGAGCCCCACAAGAGCAAAACCGTTGGAAACCAACCAACCA 2217
QY 130 HisLeuSerLysValLysLysIleProSerAspPheGluGlySerGlyTyrThrAspLeu 149
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DB 2218 -----AAACCTGTCAAGGCTCTGCCCGGGCAGGTTCACGGACCGCTG 2262
QY 150 GlnGluArgGlyAspAsnAspIleSerProPheSerGlyAspGlyGlnProPheLysAsp 169
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DB 2263 CAGGGGGAAAGGAGCCAGGGCTTCTTCCTATGCTCCCGAGACGACACTTCCAAAGAC 2322

RESULT 11
US-08-320-559-25
; Sequence 25, Application US/08320559
; Patent No. 5633135

QY 170 IlePro-----GlyLysGlyGlu----- 175
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DB 2323 AAGCCCAAGGTGAAGACGAAGGACGGCCCGGCCAGCAAGCAACCAAGCAAGCCA 2382
QY 176 AlaThrGlyProAspLeuGluGlyLysAspIleGlnThrGlyPheAlaGlyProSerGlu 195
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DB 2383 GCAGTCCCCCTCCAGTGAGAAAGAACACAGAGCTCCCTCCCTGCCCTCTTAAG 2442
QY 196 AlaGluSer-----ThrHisLeuAspThrLysLysProGlyTyr--- 208
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DB 2443 GCTCTCTCAGCCGCCAGAACCCCGAAGGACAATGTGGAGCAGGACCCCTTGACACTTT 2502
QY 209 -----AsnGluIleProGluArgGluGluAsnGlyLysThr 221
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DB 2503 GCTCTTTGTTCCCTGACTGAGACCGAGGCGGCCACCCACAGTGGCAGCGCAGGACT 2562
QY 222 IleGlyThrArgAspGluThrAlaLysGluAlaAspAlaValAspValSerLeuValGlu 241
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DB 2563 AGTGGCTGCCGCCAAGCCGTGGTGTCCAGAGGACAGCGCAAGACAGACTCCCATTTG 2622
QY 242 GlySerAsnAspIleMetGlySerThrAsnPheLysGluLeuProGlyArgGluGlyAsn 261
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DB 2623 CCTTTCAGAGACACCAAGCTGCTCTCACCGCTCAGGAGCACTCTCCCCCACAAGAGTTG 2682
QY 262 ArgVal-----AspAlaGlySerGlnAsnAla 270
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DB 2683 ATGGTGAAGATCACCTTAGACCTGCTCTCTGGATACCCAGCCTCCCGGAAGGGGAGC 2742
QY 271 HisGlnGlyValGluPheHisTyrProAlaProSerLysGluLysArgLysGlu 290
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|||
DB 2743 CGCCAGAGAAAGCAGAGATAAACAGCCCGCCGAGGGAAGACACAGCTCTGTGAAG 2802
QY 291 GlySerSerAspAlaAlaGluSerThrAsnTyrAsnGluIleProLysAsnGlyLysGly 310
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DB 2803 AGGAGCTCAGACAGCTCA-----AGCAAGTTGCCAAAAGAGAGAGGGT 2847
QY 311 SerThrArgLysGlyValAspHisSerAsnArgAsnGlnAlaThrLeuAsnGluLysGln 330
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DB 2848 GAAGCAGAAAGAGACTGTGAT-----AACAAAGAAATC 2880
QY 331 ArgPheProSerLysGlyLysSerGlnGlyLeuProIleProSerArgGlyLeuAspAsn 350
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DB 2881 AGA-----CTGGAGAAG 2892
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DB 2893 GAATCAATACAGTCATCTTCACTCTCCCAAGAAATCTTCTTAAACAAAG 2952
QY 370 -----HisGlyArgLysTyrHisTyrValProHisArgGlnAsn 382
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DB 2953 CCCTCCAGGCCCTCTCACAGTCTCTCAAGAAGGAAATGCTCCCCCGCCAGCCCGTGTCC 3012
QY 383 AsnSerThrArgAsnLysGlyMetProGlnGlyLysGlySer----- 396
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DB 3013 TGTCTCTCCAGACCGCAGCCAAAGCTGCATTAAGAGCTCAAGCGGGAAGCAGACACC 3072
QY 397 TrpGlyArgGlnPro-----HisSerAsnArgArgPheSerSer 409
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DB 3073 TGTGGCCAGGACCTCCCAAAAGTCCACAGTACCAGAGCAACCAAGAGACTCTTCC 3132
QY 410 ArgArgArgAspAspSerSerGluSerSerAspSerGlySerSerSerGlu----- 426
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DB 3133 ATTCCCAAGCAGAGAGAGTAGAGGGGAAGGCTCCAGAGGCTCTCCGAGCACAAGGTT 3192
QY 427 SerAspGlyAsp 430
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DB 3193 TCTTCGGAGAT 3204

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GENERAL INFORMATION:
APPLICANT: Croce, Carlo
APPLICANT: Canani, Eli
TITLE OF INVENTION: Diagnostics, Therapeutics and Methods for
TITLE OF INVENTION: Detection and Treatment of Acute Leukemias
TITLE OF INVENTION: Resulting from Chromosome Abnormalities in the
TITLE OF INVENTION: All-1 Region
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5633135ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/320,559
FILING DATE: 30-OCT-92
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/062,443
FILING DATE: 14 MAY 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/971,094
FILING DATE: 30-OCT-92
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/888,830
FILING DATE: 27-MAY-92
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/805,093
FILING DATE: 11-DEC-91
ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-0855
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 9391 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 421..4053
US-08-320-559-25

Alignment Scores:
Pred. No.: 0.00501 Length: 9391
Score: 137.00 Matches: 100
Percent Similarity: 34.70% Conservative: 61
Best Local Similarity: 21.55% Mismatches: 192
Query Match: 6.01% Indels: 113
DB: 1 Gaps: 17

US-09-700-696c-2 (1-430) x US-08-320-559-25 (1-9391)
QY 37 AlaLeuSerLysLeuHisAspGlnGluTyrGlyAlaLaLeuLeuArgAsnMet 56
Db 1959 GCAGTGACAACTGGCTGACCAAGTCAAGCAGCCAGCTCGCCACCAGAGGCCCCAG 2018
QY 57 GlnHisLeuMetGlyProValThrAlaLeuLysLeuLeuGluGluAsnLysGluAsn 76
Db 2019 GAGCAC---AGAGCCCCCAGCGGCGACCCAGAGAGTAAGGGCAGCAGACAGTGCAC 2075

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77 ThrProArgAsnValLeuAsn-----lleileProAlaserMetAsnTyrAlaLysAla 94
2076 GAGTC-AGGAGCATTCGAAATCAAAGATCTCTCCCC-----CTAAAGGT 2119
QY 95 HisSerLysAspLysLysLysProGlnArg-----AspSerGlnAlaGln 109
Db 2120 CC-AGCAAGAGCCCGCGGCCCGCCAGCCGGAAGCCCGCCAGGAGAGGAGTCTGAC 2178
QY 110 LysSerProValLysSerLysSerThrHisAspGlnGlnHisAsnLysLysLys 129
Db 2179 AGTCTCTCCGCGCAGCAGGAGGCCCCCAAAAGCAACCGTTGGAAACCAACACCAAC 2238
QY 130 HisLeuSerLysValLysLysLysLysLysLysLysLysLysLysLysLysLys 149
Db 2239 -----AAACCTGTCAAGGCTCTGCCCCGGCAGGTTCAACGACACGCTG 2283
QY 150 GlnGluArgGlyAspAsnAspLysSerProPheSerGlyAspGlyGlnProPheLys 169
Db 2284 CAGGGGGAAGGAGCAGCGGCTTCTTCCTATATGCTCCCGAGACACAGACTTCCAAAG 2343
QY 170 IlePro-----GlyLysGlyGlu----- 175
Db 2344 AGCCCAAGGTGAAGACGAAGAGCAGCGCCCCGGCGGAGCAGCAACGACCAAGCCCA 2403
QY 176 AlaThrGlyProAspLeuGluGlyLysAspIleGlnThrGlyPheAlaGlyProSerGlu 195
Db 2404 GCAGTGCCTCCCTCCAGTGAAGAGAGCAGCAGAGCTCCCTCCCTGCTCTCTAAAG 2463
QY 196 AlaGluSer-----ThrHisLeuAspThrLysLysProGlyTyr--- 208
Db 2464 GCTCTCTCAGGCCAGAACCCGGAAGGACAAATGTGGAGACAGGACCCCTGAGCACTT 2523
QY 209 -----AsnGluIleProGluArgGluGluAsnGlyGlyAsnThr 221
Db 2524 GCTCTTGTTCCTCTGACTGAGACCGCGGCCACCCACAGTGGCAGCGCAGCAGACT 2583
QY 222 IleGlyThrArgAspGluThrAlaLysGluAlaAspAlaValAspValSerLeuValGlu 241
Db 2584 AGTGCTGCGGCCCAAGCCGCTGGTGGTCCAGGAGGACAGCGCAAGACAGACTCCCAT 2643
QY 242 GlySerAsnAspIleMetGlySerThrAsnPheLysGluLeuProGlyArgGluGlyAsn 261
Db 2644 CTTTGAGAGACACCAAGCTGCTCTCAGCTCAGGAGACACTCTCCCTCCCAAGAGCTG 2703
QY 262 ArgVal-----AspAlaGlySerGlnAsnAla 270
Db 2704 ATGCTGAAGATCACCTCAGACCTGCTCTCTCGATACCCAGCCTCCCGGAGGAGGAG 2763
QY 271 HisGlnGlyLysValGluPheHisTyrProProAlaProSerLysLysLysLysGlu 290
Db 2764 CGCCAGAGGAAGCAGAGATTAACAGCGCCCGCAGGAGGAGGAGGAGGAGGAGGAG 2823
QY 291 GlySerSerAspAlaAlaGluSerThrAsnTyrAsnGluIleProLysAsnGlyLysGly 310
Db 2824 AGGAGCTCAGACAGCTCA-----AGCAAGTGGCCCAAAAGAGAGAGGAGT 2868
QY 311 SerThrArgLysGlyValAspHisSerAsnArgAsnGlnAlaThrLeuAsnGluLysGln 330
Db 2869 GAAGCAGAAAGAGACTGTGAT-----AACAGAGAAATC 2901
QY 331 ArgPheProSerLysGlyLysSerGlnGlyLeuProIleProSerArgGlyLeuAspAsn 350
Db 2902 AGA-----CTGGAGAG 2913
QY 351 GluIleLysAsnGluMetAspSerPheAsnGlyProSerHisGluAsnIleThr--- 369
Db 2914 GAAATCAAATCAAGTCTCTTCATCTTCTCCCAAAAGAAATCTCTTAAACAAAG 2973
QY 370 -----HisGlyArgLysTyrHisTyrValProHisArgGlnAsn 382
Db 2974 CCTCCAGGCCCTCTCAGCTCTCAAAGAGAAATGCTCCCTCCCGCCACCCCTGTGCC 3033
QY 383 AsnSerThrArgAsnLysGlyMetProGlnGlyLysGlySer----- 396

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Db 3034 TCCTCTCCAGAGCCAGCCAGCTTCACTTAAGAGGTCAAGCGGGAAGCAGACACC 3093
Qy 397 TTPGlyArgGlnPro-----HisSerAsnArgArgPheSerSer 409
Db 3094 TGTGCCAGGACCCCTCCCAAAAGTGCCAGCAGTAGTACCAAGAGCAACCAAGAGACTCTTCC 3153
Qy 410 ArgArgArgAspSerSerSerGluSerSerSerSerSerSerSerGlu----- 426
Db 3154 ATTCACAGCAGAGAGAGTAGAGGGAAGGGCTCCAGAGAGCTCTCGGAGCACAAGGGT 3213
Qy 427 SerAspGlyAsp 430
Db 3214 TCTTCGGAGAT 3225

RESULT 12
US-08-545-860D-25
; Sequence 25, Application US/08545860D
; Patent No. 6040140
; GENERAL INFORMATION:
; APPLICANT: Croce, Carlo
; APPLICANT: Canaani, Eli
; TITLE OF INVENTION: Diagnostics, Therapeutics and Methods
; TITLE OF INVENTION: for Detection and Treatment of Acute Leukemias
; TITLE OF INVENTION: Resulting from Chromosome Abnormalities in the All-1 Region
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz &
; ADDRESSEE: No. 6040140ris
; STREET: One Liberty Place, 46th floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/545,860D
; FILING DATE: 07-MAR-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/04496
; FILING DATE: 22-APR-1994
; PRIOR APPLICATION DATA: PCT/US92/10930
; APPLICATION NUMBER: PCT/US92/10930
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/327,392
; FILING DATE: 19-OCT-1994
; PRIOR APPLICATION DATA: US 08/320,559
; APPLICATION NUMBER: US 08/320,559
; FILING DATE: 11-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/062,443
; FILING DATE: 14-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/971,094
; FILING DATE: 30-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/888,839
; FILING DATE: 27-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/805,093
; FILING DATE: 11-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca Esq., Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1262
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
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; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9391 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 421..4053
; US-08-545-860D-25

Alignment Scores:
Pred. No.: 0.00501 Length: 9391
Score: 137.00 Matches: 100
Percent Similarity: 34.70% Conservative: 61
Best Local Similarity: 21.55% Mismatches: 192
Query Match: 6.01% Indels: 113
DB: 3 Gaps: 17

US-09-700-696C-2 (1-430) x US-08-545-860D-25 (1-9391)
Qy 37 AlaIleSerLysLeuHisAspGlnGluTyrGlyAlaAlaLeuIleArgAsnMet 56
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Qy 57 GlnHisIleMetGlyProValThrAlaIleLysLeuLeuGlyGluAsnLysGluAsn 76
Db 2019 GAGCAC---AGAGCCCCCGGGCGGCCACCCAGAGAGTAAGGCGCAGCAGCGCCG 2075
Qy 77 ThrProArgAsnValLeuAsn-----IleIleProAlaSerMetAsnTyrAlaLysAla 94
Db 2076 GAGTC-AGGAGCATCTCTGAATCCAAAGATCCTCCCC-----CTAAAGCT 2119
Qy 95 HisSerLysAspLysLysProGlnArg-----AspSerGlnAlaGln 109
Db 2120 CC-AGCAAGCCCCCGGGCCCCCAGCGAAGCCCCCCCCCGGAAAGAGAGAGCTGTG 2178
Qy 110 LysSerProValLysSerLysSerThrHisArgIleGlnHisAsnIleAspTyrLeuLys 129
Db 2179 AAGTCTCCGGCAGCAGCAGGAGCCCCCAAGAGCAACCTGTGGAAACCAACACCCAA 2238
Qy 130 HisLeuSerLysValLysLysIleProSerAspPheGluGlySerGlyTyrThrAspLeu 149
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Qy 150 GlnGluArgGlyAspAsnAspIleSerProPheSerGlyAspGlyGlnProPheLysAsp 169
Db 2284 CAGGGGAAAGGAGGAGCGGAGGCTTCTTCCTATGCTCCCGAGACGACAGCTTCCAAAG 2343
Qy 170 IlePro-----GlyLysGlyGlu----- 175
Db 2344 AAGCCCAAGGTGAAGAGCAAGAGGACGCGCGCGCGCGCAAGCAAGCAACCAAGCCA 2403
Qy 176 AlaThrGlyProAspLeuGluGlyLysAspIleGlnThrGlyPheAlaGlyProSerGlu 195
Db 2404 GCAGTCCCTCCCTCCAGTGAGAAGAAGACACAGAGCTCCCTCCTGCCCCCTCTAAG 2463
Qy 196 AlaGluSer-----ThrHisLeuAspThrLysLysProGlyTyr--- 208
Db 2464 GCTCTCTAGGCGCCAGAACCGGAAAGGACAAATGTGGAGACAGGACCCCTGAGCACTT 2523
Qy 209 -----AsnGluIleProGluArgGluGluAsnGlyGlyAsnThr 221
Db 2524 GCTCTTGTTCCTGACTGAGAGCCAGGCGCCACCCAGTCAGTGGCGGCGGAGAGACT 2583
Qy 222 IleGlyThrArgAspGluThrAlaLysGluAlaAspAlaValAspValSerLeuValGlu 241
Db 2584 AGTGGCTGCCGCCAAGCCGTGTGTGTGTCAGAGGAGGACCGCGCAAGACAGACTCCCAT 2643
Qy 242 GlySerAsnAspIleMetGlySerThrAsnPheLysGluLeuProGlyArgGluGlyAsn 261
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Db 2644 CTTTTCAGACACCAAGCTGCTCTACCCGCTCAGGAGACTCTCTCCCCACAAAGCTTG 2703
QY 262 ArgVal-----AspAlaGlySerGlnAsnAla 270
Db 2704 ATGCTGAAGATCAACCTAGACCTGCTCTCTCGGATACCCAGCCTCCCGGAGGGGAGC 2763
QY 271 HisGlnGlyValGluPheHisTyrProAlaProSerLysGluLysArgLysGlu 290
Db 2764 CGCAGAGGAAGACAGAGATAAACAGCCCGCCGAGGGAAGACACAGCTCTCGAAG 2823
QY 291 GlySerSerAspAlaAlaGluSerThrAsnTyrAsnGluLeuProLysAsnGlyLysGly 310
Db 2824 AGCAGCTCAGACACTCA-----AGCAGTTGCCAAAGACAGACGGT 2868
QY 311 SerThrArgLysGlyValAspHisSerAsnArgAsnGlnAlaThrLeuAsnGluLysGln 330
Db 2869 GAACGAGAAAGACTGTGAT-----AACAGAAATC 2901
QY 331 ArgPheProSerLysGlyLysSerGlnGlyLeuProfileProSerArgGlyLeuAspAsn 350
Db 2902 AGA-----CTGGAGAG 2913
QY 351 GluIleLysAsnGluMetAspSerPheAsnGlyProSerHisGluAsnIleLeuThr--- 369
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QY 370 -----HisGlyArgLysTyrHisTyrValProHisArgGlnAsn 382
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QY 410 ArgArgArgAspAspSerSerGluSerSerAspSerGlySerSerSerGlu----- 426
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QY 427 SerAspGlyAsp 430
Db 3214 TCTTCGGAGAT 3225

RESULT 13
PCT-US94-04496-25
Sequence 25, Application PC/TUS9404496
GENERAL INFORMATION:
APPLICANT: Croce, Carlo
APPLICANT: Canadani, Eli
TITLE OF INVENTION: Diagnostics, Therapeutics and Methods
TITLE OF INVENTION: for Detection and Treatment of Acute Leukemias
TITLE OF INVENTION: Resulting from Chromosome Abnormalities in the ALL-1
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSER: Woodcock, Washburn, Kurtz, Mackiewicz &
ADDRESSER: Norris
STREET: One Liberty Place, 46th floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/04496
FILING DATE:
CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:
NAME: DeLuca Esq., Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-1242
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 9391 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 421...4053
PCT-US94-04496-25
Alignment Scores:
Pred. No.: 0.00501 Length: 9391
Score: 137.00 Matches: 100
Percent Similarity: 34.70% Conservative: 61
Best Local Similarity: 21.55% Mismatches: 192
Query Match: 6.01% Indels: 113
DB: 5 Gaps: 17
US-09-700-696C-2 (1-430) x PCT-US94-04496-25 (1-9391)
QY 37 AlaIleSerLysLeuHisAspGlnGluTyrGlyAlaAlaLeuIleArgAsnMet 56
Db 1959 GCAGCTGGAGCACTGCTGACCAAGTCAGCCAGCCAGCTGCCACACAGGGCCCCAG 2018
QY 57 GlnHisIleMetGlyProValThrAlaIleLysLeuLeuGluGluAsnLysGluAsn 76
Db 2019 GAGCAC---AGAGCCCCAGCGGCAGCCAGAGAGTAAGGGCAGCAGAGTCAC 2075
QY 77 ThrProArgAsnValLeuAsn-----IleIleProAlaSerMetAsnTyrAlaLysAla 94
Db 2076 GAGTC-AGGAGCATCTTGAATCCAAAGATCTCTCCC-----CTAAAGCT 2119
QY 95 HisSerLysAspLysLysLysProGlnArg-----AspSerGlnAlaGln 109
Db 2120 CC-AGCAAGCCCCCGGGCCGCCAGCCAGAGCCCCCCCCAGAGAGAGAGCTGTAC 2178
QY 110 LysSerProValLysSerLysSerThrHisArgIleGlnHisAsnIleAspTyrLeuLys 129
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Db 2239 -----AACTCTCAAGGCTCTGCCCGGCGAGGTTTCAGGACGACCTG 2283
QY 150 GlnGluArgGlyAspAsnAspLysSerProPheSerGlyAspGlyGlnProPheLysAsp 169
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Db 2404 GCAGTGCCCCCTCCAGTGAGAGAGAGAGACACAGAGAGTCCCTCCCTGCCCTCTTAAG 2463
QY 196 AlaGluSer-----ThrHisLeuAspThrLysLysProGlyTyr--- 208
Db 2464 GCTCTCAGGCCCCAGAACCCCGAAGGAGCAATATGGAGGACAGGACCCCTCAGCACTTT 2523
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Db 2524 GCTCTGTTCCTGACTGAGAGCGCAGGGCCGCCACCCACAGTCAGTGGCAGCGCAGGACT 2583

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QY 222 IleGlyThrArgAspGluThrAlaLysGluAlaAspAlaValSerLeuValGlu 241
Db 2584 AGTGGCTGCCCAAGCCGCGTGGTCCAGGAGACAGCCGCAAGACACATCCCATG 2643
QY 242 GlySerAsnAspIleMetGlySerThrAsnPhelLysGluLeuProGlyArgGluGlyAsn 261
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QY 271 HisGlnGlyLysValGluPheHisTyrProProAlaProSerLysGluLysArgLysGlu 290
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QY 291 GlySerSerAspAlaAlaGluSerThrAsnTyrAsnGluIleProLysAsnGlyLysGly 310
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QY 311 SerThrArgLysGlyValAspHisSerAsnArgAsnGlnAlaThrLeuAsnGluLysGln 330
Db 2869 GAAGCAGAAAGAGAGCTGTGAT-----AACCAAGAAATC 2901
QY 331 ArgPheProSerLysGlyLysSerGlnGlyLeuProIleProSerArgGlyLeuAspAsn 350
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QY 351 GluIleLysAsnGluMetAspSerPheAsnGlyProSerHisGluAsnIleLeuThr--- 369
Db 2914 GAAATCAAAATCAGACGATCTTCATCTTCATCTCCACAAAGAAATCTTTAAACAAAG 2973
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Db 3094 TGTGGCCAGGACCTCTCCAAAAGTGGCCAGCAGTACCAGACCAACCAAGAACTCTTCC 3153
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Db 3214 TCTTCGGAGAT 3225
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RESULT 14
US-08-568-459A-1
; Sequence 1, Application US/08568459A
; Patent No. 5849306
; GENERAL INFORMATION:
; APPLICANT: Sim, Kim L.
; APPLICANT: Chitnis, Chetan
; APPLICANT: Miller, Louis H.
; APPLICANT: Peterson, David S.
; APPLICANT: Su, Xin-zhaun
; APPLICANT: Wellens, Thomas E.
; TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
; TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobs Martens Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: California
; COUNTRY: US
; ZIP: 92660
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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/568,459A
; APPLICATION NUMBER: 07-DEC-1995
; FILING DATE: 07-DEC-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Israel, Ned
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: NIH121.001CPI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4084 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Plasmodium vivax
; US-08-568-459A-1
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Alignment Scores:
Pred. No.: 0.00256 Length: 4084
Score: 134.50 Matches: 97
Percent Similarity: 36.42% Conservative: 80
Best Local Similarity: 19.96% Mismatches: 220
Query Match: 5.90% Indels: 89
DB: 2 Gaps: 21
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US-09-700-696C-2 (1-430) x US-08-568-459A-1 (1-4084)

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QY 22 TyrProLysSerThrGlyAsnLysGlyPheGluAspGlyAspAlaIleSerLysLeu 41
Db 1784 TAT-----GATATCTAAACACAG--- 1801
QY 42 HisAspGlnGluGluTyrGlyAlaAlaLeuIleArgAsnAsnMetGlnHisIleMetGly 61
Db 1802 ---GAGTTAGATGAATTTAACGAGGTGGCTTTTGAGAAATGAATTAACAAACGTGATGGT 1858
QY 62 ProValThrAlaIleLysLeuLeuGly---GluGluAsnLysGluAsnThrProArgAsn 80
Db 1859 GCATATATTGAGTTATGCGTTTGTTCGTTGAAGAGGCTAAAAAAATACTCAGGAAGTT 1918
QY 81 ValLeuAsnIleIleProAlaSerMetAsnTyrAlaLysAlaHisSerLysAspLysLys 100
Db 1919 GTGACAAATGTGCAATGCTCTAAATCTCAGGCC---ACCAATTCAAATCCGATAAGT 1975
QY 101 LysProGlnArgAspSerGlnAlaGlnLysSerProValLysSerLysSerThrHisArg 120
Db 1976 CAGCCTGTAGATAGTAGTAAGCGGAGAGGTCTCA-----GGAGATCTACGCAT--- 2026
QY 121 IleGlnHisAsnIleAspTyrLeuLysHisLeuSerLysVal---LysLysIleProSer 139
Db 2027 -----GGAAATGTTTAAACAGTGGCCCAAGATGTTCTCACCACAGGTAAAGCTGTACGGGG 2080
QY 140 AspPheGluGlySerGlyTyrThrAspLeuGln-----GluArgLysAspAsnAsp 156
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QY 157 IleSerProPheSerGlyAspGlyGlnProPheLysAspIleProGlyLysGlyGlu--- 175
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QY 193 ProSerGluAlaGluSerThrHisLeuAspThrLysLysProGly----- 207
Db 2258 AGTCGACCTTCGAGTCCACC-----GTGGAAGCAAAATAGCCCGAGTGATGATCAATGCGAAC 2314
QY 208 -----TyrAsnGluIle 211
Db 2315 AGTCGATCTATACCTGAGTGGTGGTGAAGAACCCCATTTGTTACCCCTATATGTTG 2374
QY 212 ProGluArgGluAsnGlyGlyAsn-----Thr 221
Db 2375 AGGCATTCGAAGACAACTAGTATGATGATGATGCGGAAATCAATGGCGATCTCTGAT 2434
QY 222 IleGlyThrArgAspGluThrAlaLysGluAlaAspAlaValAspValSerLeuValGlu 241
Db 2435 TCAATAGTAGTACAGCGGGAAGGGCAAGATGATGATGCGAAGGCTACTAA 2494
QY 242 GlySerAsnAspIleMetGlySerThrAsnPheLysGluLeuProGlyArgGluGlyAsn 261
Db 2495 GATAGTAGTAATAGTTTCAGATGCTACGAGC-----TCTGCTACGGGTGAT 2539
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QY 282 AlaProSerLysLysArgLysGlyGlySerSer-----AspAlaAlaGluSer 298
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QY 299 ThrAsnTyrAsnGluIleProLysAsnGlyLysGlySerThr-----ArgLysGly 315
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QY 334 SerLysGlyLysSerGlnGlyLeuProIleProSerArgGly-----LeuAspAsnGlu 351
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QY 387 -----AsnLysGlyMetProGlnGlyLysGlySerTyrGlyArgGlnProHisSer 403
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RESULT 15

US-08-487-826B-1

; Sequence 1, Application US/08487826B

; Patent No. 5933827

; GENERAL INFORMATION:

; APPLICANT: Sim, Kim L.

; APPLICANT: Chitnis, Chetan

; APPLICANT: Miller, Louis H.

```
; APPLICANT: Peterson, David S.
; APPLICANT: Su, Xin-zhaun
; APPLICANT: Wellem, Thomas E.
; TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
; TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobb Martens Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: California
; COUNTRY: US
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,826B
; FILING DATE: 10-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Israel, Ned
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: NIH121.001CP1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4084 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Plasmodium vivax
; US-08-487-826B-1
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Alignment Scores:

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|------------------------|---------|---------------|------|
| Pred. No.: | 0.00256 | Length: | 4084 |
| Score: | 134.50 | Matches: | 97 |
| Percent Similarity: | 36.42% | Conservative: | 80 |
| Best Local Similarity: | 19.96% | Mismatches: | 220 |
| Query Match: | 5.90% | Indels: | 89 |
| DB: | 2 | Gaps: | 21 |

US-09-700-696C-2 (1-430) x US-08-487-826B-1 (1-4084)

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QY 2 AsnLysGluTyrSerIleSerAsnLysGluAsnThrHisAsnGlyLeuArgMetSerIle 21
Db 1724 ANTAATTCATAGTGTAAACCCAGAAAGGTTTCAGACGCGAGGTATCGTAATCTCT 1783
QY 22 TyrProLysSerThrGlyAsnLysGlyPheGluAspGlyAspAlaIleSerLysLeu 41
Db 1784 TAT-----GATATACTAAACAG--- 1801
QY 42 HisAspGlnGluTyrGlyAlaAlaLeuIleArgAsnAsnMetGlnHisIleMetGly 61
Db 1802 ---GAGTTAGATGAATTTAACGAGGTGGCTTTTGAGAAATTAACAAACGCTGATGT 1858
QY 62 ProValThrAlaIleLysLeuLeuGly---GluGluAsnLysGluAsnThrProArgAsn 80
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Qy 121 IleGlnHisAsnIleAspTyrLeuLysHisLeuSerLysVal-----LysLysIleProSer 139
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Db 2201 ACTCAAGCGTTACAGGTATTGCCAAGCTCGAAAGGAA---AACTTAGCGCATCAAT 2257
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Db 2315 AGTGCATCTATACCTGTAGTGTAGTGGTGGAACCCATTGGTAACCCCTATAATGGTTG 2374
Qy 212 ProGluArgGluGluAsnGlyGlyAsn-----Thr 221
Db 2375 AGGCAITTCGAAAGCAATAGTAGATGATGCGATGGGACTCGGGAATCAATGGCGAATCCTGAT 2434
Qy 222 IleGlyThrArgAspGluThrAlaLysGluAlaAspAlaValAspValSerLeuValGlu 241
Db 2435 TCAATAGTAAGGTGAGACGGGAAAGGGCAAGATAATGATATGGCGAAGGCTACTAAA 2494
Qy 242 GlySerAsnAspIleMetGlySerThrAsnPhelLysGluLeuProGlyArgGluGlyAsn 261
Db 2495 GATAGTAGTAATAGTTCAGATGGTACCAGC-----TCTGCTACGGGTGAT 2539
Qy 262 ArgValAspAlaGlySerGlnAsnAlaHisGlnGlyLysValGluPheHisTyrProPro 281
Db 2540 ACTACTGATCGAGTTGATGGGAAATTAATAAGGTGTTCTGAGGATAGGGATAAAACT 2599
Qy 282 AlaProSerLysGluLysArgLysGluGlySerSer-----AspAlaAlaGluSer 298
Db 2600 GTAGGAAGTAAAGATGAGGAGGGGGGAGAGATAACTCTGCAAAATAGGATGCGGACTGTA 2659
Qy 299 ThrAsnTyrAsnGluIleProLysAsnGlyLysGlySerThr-----ArgLysGly 315
Db 2660 GTTGGTCAGGATAGAAATCTGTGAGAACAGCGCTGGTGTAGCACTAATGATAGATCAAAA 2719
Qy 316 ValAspHisSerAsnArgAsnGlnAlaThrLeuAsnGluLysGlnArg-----PhePro 333
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Qy 334 SerLysGlyLysSerGlnGlyLeuProIleProSerArgGly-----LeuAspAsnGlu 351
Db 2780 GCGCTAAGTAAACCCGAAAGTTTAGAATCAACAGAAAGTGGAGATAGAACTACTAATGAT 2839
Qy 352 IleLysAsnGluMetAspSerPheAsnGlyProSerHisGluAsnIleIleThrHisGly 371
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Qy 372 ArgLysTyrHisTyrValProHisArgGlnAsnAsnSerThrArg----- 386
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Db 2960 GGACATGACAGGATAGCATCAAAAATGATAAAGACAGAA-----AGGAGAAAGCATATG 3013
Qy 404 AsnArg---ArgPheSerSerArgArgAspAspSerSerGluSerSerAspSerGly 422
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Qy 423 SerSerSerGluSerAsp 428
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Db 3074 AGTAATGAAAAATTAGAT 3091

Search completed: November 30, 2003, 02:11:35
Job time : 115 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: November 30, 2003, 00:14:26 ; Search time 423 Seconds
(without alignments)
3349.212 Million cell updates/sec

Title: US-09-700-696C-2

Perfect score: 2279

Sequence: 1 VNKEYSISKENTHNGLRMS.....RRDSSSSSSGSSSSSDGD 430

Scoring table: BLOSUM62

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2190069 seqs, 1647345023 residues

Total number of hits satisfying chosen parameters: 4380138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=Published Applications NA -QEXT=fastCap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPTXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCLIGN=200 -THR SCORE=pct -THR MAX=100
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Database : Published Applications NA:

- 1: /cgn2_6/prodata/2/pubpna/US07_PUBCOMB.seq:
- 2: /cgn2_6/prodata/2/pubpna/PCT_NEW_PUB.seq:
- 3: /cgn2_6/prodata/2/pubpna/US06_NEW_PUB.seq:
- 4: /cgn2_6/prodata/2/pubpna/US06_PUBCOMB.seq:
- 5: /cgn2_6/prodata/2/pubpna/US07_NEW_PUB.seq:
- 6: /cgn2_6/prodata/2/pubpna/PCTUS_PUBCOMB.seq:
- 7: /cgn2_6/prodata/2/pubpna/US08_NEW_PUB.seq:
- 8: /cgn2_6/prodata/2/pubpna/US08_PUBCOMB.seq:
- 9: /cgn2_6/prodata/2/pubpna/US09A_PUBCOMB.seq:
- 10: /cgn2_6/prodata/2/pubpna/US09B_PUBCOMB.seq:
- 11: /cgn2_6/prodata/2/pubpna/US09C_PUBCOMB.seq:
- 12: /cgn2_6/prodata/2/pubpna/US09_NEW_PUB.seq:
- 13: /cgn2_6/prodata/2/pubpna/US10A_PUBCOMB.seq:
- 14: /cgn2_6/prodata/2/pubpna/US10B_PUBCOMB.seq:
- 15: /cgn2_6/prodata/2/pubpna/US10_NEW_PUB.seq:
- 16: /cgn2_6/prodata/2/pubpna/US60_NEW_PUB.seq:
- 17: /cgn2_6/prodata/2/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-----------------------------------|
| 1 | 2276 | 99.9 | 1575 | 12 | US-10-311-840-2 Sequence 2, Appli |

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|----|-------|------|---------|----|---------------------------------------|
| 2 | 2276 | 99.9 | 1662 | 12 | US-10-311-840-3 Sequence 3, Appli |
| 3 | 2276 | 99.9 | 1876 | 12 | US-09-794-422-33 Sequence 33, Appl |
| 4 | 2276 | 99.9 | 1969 | 12 | US-09-794-422-45 Sequence 45, Appl |
| 5 | 2276 | 99.9 | 2019 | 12 | US-09-794-422-5 Sequence 5, Appli |
| 6 | 2276 | 99.9 | 2112 | 12 | US-09-794-422-7 Sequence 7, Appli |
| 7 | 983.5 | 43.2 | 1692 | 12 | US-09-794-422-3 Sequence 3, Appli |
| 8 | 938.5 | 41.2 | 1655 | 12 | US-09-794-422-1 Sequence 1, Appli |
| 9 | 148.5 | 6.5 | 8201 | 12 | US-10-363-798-1 Sequence 1, Appli |
| 10 | 148 | 6.5 | 5721 | 10 | US-09-785-770A-15 Sequence 15, Appl |
| 11 | 148 | 6.5 | 8121 | 10 | US-09-785-770A-14 Sequence 14, Appl |
| 12 | 140 | 6.1 | 2673 | 14 | US-10-153-668-301 Sequence 301, App |
| 13 | 140 | 6.1 | 4839 | 12 | US-10-101-510-398 Sequence 398, App |
| 14 | 139 | 6.1 | 35465 | 14 | US-10-161-572-6 Sequence 6, Appli |
| 15 | 139 | 6.1 | 36991 | 14 | US-10-161-572-8 Sequence 8, Appli |
| 16 | 137 | 6.0 | 9330 | 14 | US-10-205-823-263 Sequence 263, App |
| 17 | 134.5 | 5.9 | 4084 | 13 | US-10-153-273-1 Sequence 1, Appli |
| 18 | 134 | 5.9 | 1446 | 14 | US-10-156-761-4465 Sequence 4465, Ap |
| 19 | 134 | 5.9 | 2254 | 14 | US-10-198-846-13929 Sequence 13929, A |
| 20 | 134 | 5.9 | 9025608 | 14 | US-10-156-761-1 Sequence 1, Appli |
| 21 | 133.5 | 5.9 | 1960 | 9 | US-09-864-761-4620 Sequence 4620, Ap |
| 22 | 133.5 | 5.9 | 7058 | 12 | US-10-287-218-38 Sequence 38, Appl |
| 23 | 131 | 5.7 | 2025 | 10 | US-09-834-975-822 Sequence 822, App |
| 24 | 130.5 | 5.7 | 1450 | 13 | US-10-001-835-66 Sequence 66, Appl |
| 25 | 130.5 | 5.7 | 3316 | 12 | US-10-133-013-166 Sequence 166, App |
| 26 | 130.5 | 5.7 | 5469 | 12 | US-10-341-434-94 Sequence 94, Appl |
| 27 | 130 | 5.7 | 1501 | 12 | US-10-017-161-2097 Sequence 2097, Ap |
| 28 | 129.5 | 5.7 | 2454 | 9 | US-09-962-436-563 Sequence 563, App |
| 29 | 129.5 | 5.7 | 2454 | 14 | US-10-175-523-55 Sequence 55, Appl |
| 30 | 129.5 | 5.7 | 2480 | 14 | US-10-060-036-4548 Sequence 4548, Ap |
| 31 | 129.5 | 5.7 | 2491 | 14 | US-10-084-817-352 Sequence 352, App |
| 32 | 129.5 | 5.7 | 2885 | 14 | US-10-198-846-13303 Sequence 13303, A |
| 33 | 127.5 | 5.6 | 1763 | 12 | US-10-017-161-2323 Sequence 1, Appli |
| 34 | 127.5 | 5.6 | 3708 | 12 | US-09-758-036-1 Sequence 3423, Ap |
| 35 | 127.5 | 5.6 | 4840 | 10 | US-09-880-107-3423 Sequence 63, Appl |
| 36 | 127 | 5.6 | 1066 | 11 | US-09-746-660A-63 Sequence 2161, Ap |
| 37 | 127 | 5.6 | 2154 | 10 | US-09-738-626-2161 Sequence 22571, A |
| 38 | 127 | 5.6 | 2612 | 12 | US-10-029-386-22571 Sequence 253, App |
| 39 | 127 | 5.6 | 2636 | 14 | US-10-153-668-253 Sequence 295, App |
| 40 | 127 | 5.6 | 4215 | 14 | US-10-037-270-295 Sequence 29, Appl |
| 41 | 127 | 5.6 | 4380 | 12 | US-10-094-466-29 Sequence 6, Appli |
| 42 | 127 | 5.6 | 5331 | 10 | US-09-764-176-6 Sequence 188, App |
| 43 | 127 | 5.6 | 11167 | 12 | US-10-252-157-188 Sequence 1, Appli |
| 44 | 127 | 5.6 | 3309400 | 10 | US-09-738-626-1 Sequence 1739, Ap |
| 45 | 126.5 | 5.6 | 2390 | 14 | US-10-102-524-1739 |

ALIGNMENTS

RESULT 1

US-10-311-840-2
; Sequence 2, Application US/10311840
; Publication No. US20030175808A1
; GENERAL INFORMATION:
; APPLICANT: KUROKAWA, Tomofumi
; APPLICANT: YAMADA, Takao
; APPLICANT: MORIMOTO, Shigetomo
; TITLE OF INVENTION: No. US20030175808A1 Protein and its DNA
; FILE REFERENCE: 2738USOP
; CURRENT APPLICATION NUMBER: US/10/311,840
; PRIOR FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: PCT/JP01/05263
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: JP 2000-191088
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 2
; LENGTH: 1575
; TYPE: DNA
; ORGANISM: Human
US-10-311-840-2

Alignment Scores: 2.22e-213 Length: 1575
Pred. No.: 1

Score: 2276.00 Matches: 429
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.77% Mismatches: 0
Query Match: 99.87% Indels: 0
DB: 12 Gaps: 0

US-09-700-696C-2 (1-430) x US-10-311-840-2 (1-1575)

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Db ATTTATCTTAAGTCAACTGGGAAATAAAGGGTTTGGAGATGGAGATGTCTATCAGCAA 405

QY 41 LeuHisAspGlnGluTyrGlyAlaAlaLeuIleArgAsnMetGlnHisIleMet 60
Db CTACATGACCAAGAAATATGGCGAGCTCTCATCAGAAATACATGCAACATATATG 465

QY 61 GlyProValThrAlaIleLysLeuLysGlyGluGluAsnLysGluAsnThrProArgAsn 80
Db GGGCCAGTGAATCGGATTAATCTCTGGGGAGAAACAAAGAGAAACACACCTTAGGAAT 525

QY 81 ValLeuAsnIleLeuProAlaSerMetAsnTyrAlaLysAlaHisSerLysAspLysLys 100
Db GTTCTAAACATAATCCAGCAGATGATGATATATCTAAAGCACACTCGAAGGATAAAAG 585

QY 101 LysProGlnArgAspSerGlnAlaGlnLysSerProValLysSerLysSerThrHisArg 120
Db AAGCCTCAAGAGATTCACCAAGCCAGAAAAGTCCAGTAAAGCAAAAGCAACCATCGT 645

QY 121 IleGlnHisAsnIleAspTyrLeuLysHisLeuSerLysValLysLysIleProSerAsp 140
Db ATTCAACACACAACTGACTACCTAAACATCTCTCAAAAGCTCAAAATAATCCCCAGTAT 705

QY 141 PheGluGlySerGlyTyrThrAspLeuGlnGluArgGlyAspAsnAspIleSerProPhe 160
Db TTGTGAAGGACGGTTTATACAGATCTTCAAGAGAGAGGGACATGATATATCTCTCTTC 765

QY 161 SerGlyAspGlyGlnProPheLysAspIleProGlyLysGlyGluAlaThrGlyProAsp 180
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QY 181 LeuGluGlyLysAspIleGlnThrGlyPheAlaGlyProSerGluAlaGluSerThrHis 200
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QY 201 LeuAspThrLysLysProGlyTyrAsnGluIleProGluArgGluGluAsnGlyGlyAsn 220
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QY 221 ThrIleGlyThrArgAspGluThrAlaLysGluAlaAspAlaValAspValSerLeuVal 240
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QY 241 GluGlySerAsnAspIleMetGlySerThrAsnPheLysGluLeuProGlyArgGluGly 260
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QY 281 ProAlaProSerLysGluLysArgLysGluGlySerSerAspAlaAlaGluSerThrAsn 300
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QY 301 TyrAsnGluIleProLysAsnGlyLysGlySerThrArgLysGlyValAspHisSerAsn 320
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QY 321 ArgAsnGlnAlaThrLeuAsnGluLysGlnArgPheProSerLysGlyLysSerGlnGly 340

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QY 361 GlyProSerHisGluAsnIleLeuThrHisGlyArgLysTyrHisTyrValProHisArg 380
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QY 401 ProHisSerAsnArgArgPheSerSerArgArgArgAspAspSerSerGluSerSerAsp 420
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QY 421 SerGlySerSerGluSerAspGlyAsp 430
Db AGTGGCAGTTCAAGTGAGAGCGATGTGAC 1575

RESULT 2
US-10-311-840-3
; Sequence 3, Application US/10311840
; Publication No. US20030175808A1
; GENERAL INFORMATION:
; APPLICANT: KUROKAWA, Tomofumi
; APPLICANT: YAMADA, Takao
; APPLICANT: MORIMOTO, Shigeto
; TITLE OF INVENTION: No. US20030175808A1 Protein and its DNA
; FILE REFERENCE: 2738USOP
; CURRENT APPLICATION NUMBER: US/10/311,840
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: PCT/JP01/05263
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: JP 2000-191088
; PRIOR FILING DATE: 2000-06-21
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 3
; LENGTH: 1662
; TYPE: DNA
; ORGANISM: Human
US-10-311-840-3

Alignment Scores:
Pred. No.: 2,38e-213 Length: 1662
Score: 2276.00 Matches: 429
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.77% Mismatches: 0
Query Match: 99.87% Indels: 0
DB: 12 Gaps: 0

US-09-700-696C-2 (1-430) x US-10-311-840-3 (1-1662)

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QY 41 LeuHisAspGlnGluTyrGlyAlaAlaLeuIleArgAsnMetGlnHisIleMet 60
Db CTACATGACCAAGAAATATGGCGAGCTCTCATCAGAAATAACATGCAACATATAATG 472

QY 61 GlyProValThrAlaIleLysLeuLysGlyGluGluAsnLysGluAsnThrProArgAsn 80
Db GGGCCAGTGAATCGGATTAATCTCTGGGGAGAAACAAAGAGAAACACACCTTAGGAAT 532

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Db 593 AAGCCTCAAGAGATCCCAAGCCCAAGAAAGTCCAGTAAAGCAAGCAAGCAAGCCATCGT 652
Qy 121 IleGlnHisAsnIleAspTyrLeuLysHisLeuSerLysValLysLysIleProSerAsp 140
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Qy 181 LeuGluGlyLysAspIleGlnThrGlyPheAlaGlyProSerGluAlaGluSerThrHis 200
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Qy 201 LeuAspThrLysLysProGlyTyrAsnGluIleProGluArgGluGluAsnGlyGlyAsn 220
Db 893 CTTGACACAAAAGCCAGGTTATATGAGATCCAGAGAGAGAGAAATGGTGGAAAT 952
Qy 221 ThrIleGlyThrArgAspGluThrAlaLysGluAlaAspAlaValSerLeuVal 240
Db 953 ACCATTGGAACTAGGATGAACTGCGAAAGAGGACAGTCTGTGTATGTGACGCTTGTA 1012
Qy 241 GluGlySerAsnAspIleMetGlySerThrAsnPhelLysGluLeuProGlyArgGluGly 260
Db 1013 GAGGGCAGCAAGCATATCATCGGTAGTACCAATTTTAAAGAGCTCCCTGGAAGAGAAGA 1072
Qy 261 AsnArgValAspAlaGlySerGlnAsnAlaHisGlnGlyLysValGluPheHisTyrPro 280
Db 1073 AACAGAGTGGATGCTGGCAGCCAAATGCTCACCAGGGAAGGTGTAGTTTCTATCCCT 1132
Qy 281 ProAlaProSerLysGluLysArgLysGluGlySerSerAspAlaAlaGluSerThrAsn 300
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Qy 301 TyrAsnGluIleProLysAsnGlyLysGlySerThrArgLysGlyValAspHisSerAsn 320
Db 1193 TATATATGAAATCTCTAAATGGCAAGGAGTACCAAGAGGTTGTAGTATCTTCTAT 1252
Qy 321 ArgAsnGlnAlaThrLeuAsnGluLysGlnArgPheProSerLysGlyLysSerGlnGly 340
Db 1253 AGGAACCAAGCAACCTTAAATGAAACAAAGGTTTCTTGTAGTAAAGGCAAAAGTCAGGGC 1312
Qy 341 LeuProIleProSerArgGlyLeuAspAsnGluIleLysAsnGluMetAspSerPheAsn 360
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Qy 361 GlyProSerHisGluAsnIleThrHisGlyArgLysTyrHisTyrValProHisArg 380
Db 1373 GGCCCCAGTCATGAGATATAATAACACATGCCAGAAATATCATTTATGATACCCACAGA 1432
Qy 381 GlnAsnAsnSerThrArgAsnLysGlyMetProGlnGlyLysGlySerTyrGlyArgGln 400
Db 1433 CAAATATTTCTACAGGAATTAAGGATGTCACCAAGGAAAGGCTCTCTGGGGTAGACAA 1492
Qy 401 ProHisSerAsnArgPheSerSerArgArgAspAspSerSerGluSerSerAsp 420
Db 1493 CCCCATTTCAACAGAGGTTTGTAGTTCCGTAGAGGAGTGCACATGATGATCATCTGAC 1552
Qy 421 SerGlySerSerGluSerAspGlyAsp 430
Db 1553 AGTGGCAGTTCAAGTGAGAGCGATGGTAC 1582

RESULT 3

US-09-794-422-33

; Sequence 33, Application US/09794422
; Publication No. US20030166239A1
; GENERAL INFORMATION:
; APPLICANT: Brown, Thomas A.
; APPLICANT: De Wet, Jeffrey R.
; APPLICANT: Gowen, Lori C.
; APPLICANT: Hames, Lynn M.
; TITLE OF INVENTION: Mammalian Osteoregulins
; FILE REFERENCE: PC10445
; CURRENT APPLICATION NUMBER: US/09/794,422
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 60/185,617
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 60/234,500
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33
; LENGTH: 1876
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-794-422-33

Alignment Scores:

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|------------------------|-----------|---------------|------|
| Pred. No.: | 2,78e-213 | Length: | 1876 |
| Score: | 2276.00 | Matches: | 429 |
| Percent Similarity: | 100.00% | Conservative: | 1 |
| Best Local Similarity: | 99.77% | Mismatches: | 0 |
| Query Match: | 99.87% | Indels: | 0 |
| DB: | 12 | Gaps: | 0 |

US-09-700-696C-2 (1-430) x US-09-794-422-33 (1-1876)

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Db 238 CTGAATAAAGATATAGTATAGTAAACAAGAGATACTCAATGGGCTCAGGATGTCA 297
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Db 298 ATTATCTTAAGTCACTGGGAATAAGGTTTGAAGTTGGAGATGATGCTATCAGCAA 357
Qy 41 LeuHisAspGlnGluTyrGlyAlaAlaLeuIleArgAsnAsnMetGlnHisIleMet 60
Db 358 CTACATGACCAAGAAGATATGGCGAGCTCTCATCAGAAATAACATGCAACATATAATG 417
Qy 61 GlyProValThrAlaIleLysLeuGlyGluAsnLysGluAsnThrProArgAsn 80
Db 418 GGGCCAGTGACTGCCATTAAACTCTCTGGGGAGAAACAAAGAGAACACACTTAGGAAT 477
Qy 81 ValLeuAsnIleIleProAlaSerMetAsnTyrAlaLysAlaHisSerLysAspLysLys 100
Db 478 GTTCTAAACATATCCAGCAAGTATGAAATTATGCTAAAGCACACTCGAAGGATAAAAG 537
Qy 101 LysProGlnArgAspSerGlnAlaGlnLysSerProValLysSerLysSerThrHisArg 120
Db 538 AAGCCTCAAGAGATTTCCCAAGCCAGAAAGTCCAGTAAAGCAAAAGCAAGCACCATCGT 597
Qy 121 IleGlnHisAsnIleAspTyrLeuLysHisLeuSerLysValLysLysIleProSerAsp 140
Db 598 ATTCAACACACATTTGACTACCTAAACATCTCTCAAAAGTCAAAAATCCCAAGTAT 657
Qy 141 PheGluGlySerGlyTyrThrAspLeuGlnGluArgGlyAspAsnAspIleSerProPhe 160
Db 658 TTTGAAGGCGAGCGTTATACAGATCTTCAAGAGAGAGGGGACCAATGATATATCTCTTC 717
Qy 161 SerGlyAspGlyGlnProPheLysAspIleProGlyLysGlyGluAlaThrGlyProAsp 180
Db 718 AGTGGGACGGCCAAACCTTTTAAAGACATCTCTGTAAGGAGAGAGCTACTGGTCTCTGAC 777
Qy 181 LeuGluGlyLysAspIleGlnThrGlyPheAlaGlyProSerGluAlaGluSerThrHis 200
Db 778 CTAGAGGCAAGATATTCAAACAGGGTTTGCAGGCCCAAGTGAAGCTGAGAGTACTCAT 837

```
QY 201 LeuAspThrLysLysProGlyTyrAsnGluLeuProGluArgGluGluAsnGlyGlyAsn 220
Db 838 CTTGACACAAAAAGCCAGGTATATAATGAGATCCAGACAGAGAGAAATGGTGAAT 897
QY 221 ThrIleGlyThrArgAspGluThrAlaLysGluAlaAspAlaValSerLeuVal 240
Db 898 ACCATTGGAACTAGGATGAACCTGCGAAGAGGAGCATGCTGTTGATGACGCTTGTGA 957
QY 241 GluGlySerAsnAspIleMetGlySerThrAsnPhelLysGluLeuProGlyArgGluGly 260
Db 958 GAGGCGACGACGATATCATGGGTAGTACCAATTTTAAGGAGCTCCCTGGAGAGAGGA 1017
QY 261 AsnArgValAspAlaGlySerGlnAsnAlaHisGlnGlyLysValGluPheHisTyrPro 280
Db 1018 AACAGAGTGTGATGCTGCAGCCCAAAATGCTCACCAAGGGAAGGTGTGATTTTCATTAC 1077
QY 281 ProAlaProSerLysGluLysArgLysGluGlySerThrArgLysGlyValAspHisSerAsn 300
Db 1078 CTTGCACCTTCAAAAGAGAAAGAAAGAAAGAGGCTAGTGTGATGCTGAAGTACCAC 1137
QY 301 TyrAsnGluLeuProLysAsnGlyLysGlySerThrArgLysGlyValAspHisSerAsn 320
Db 1138 TATAATGAATTCCTAAAAATGGCAAGGCGAGTACCAGAAAGGCTGTAGATCATTTCTAAT 1197
QY 321 ArgAsnGlnAlaThrLeuAsnGluLysGlnArgPheProSerLysGlyLysSerGlnGly 340
Db 1198 AGAACCAAGCAACCTTAAATGAATAAACAAGAGTTTCTTAGTAAAGGCAAAAGTCAGGGC 1257
QY 341 LeuProIleProSerArgGlyLeuAspAsnGluLeuLysAsnGluMetAspSerPheAsn 360
Db 1258 CTGCCCATCTTCTCGTGTCTTGATAATGAATCAAAACCGAATGGATTCCTTTAAT 1317
QY 361 GlyProSerHisGluAsnIleThrHisGlyArgLysTyrHisTyrValProHisArg 380
Db 1318 GGCCCCAGTCATGAGATATAATAACACATGGCAGAGAAATATCATTTATGTACCCACAGA 1377
QY 381 GlnAsnAsnSerThrArgAsnLysGlyMetProGlnGlyLysGlySerTyrGlyArgGln 400
Db 1378 CAAAAATATCTACACGGAATAAGGTATGCCAAGGGAAGGCTCCTGGGGTAGACAA 1437
QY 401 ProHisSerAsnArgPheSerSerArgArgAspAspSerSerGluSerSerAsp 420
Db 1438 CCCCATTTCAACAGGAGTTTGTCTCCGTAGAAGGATGACAGTGTAGTCAATCTGTAC 1497
QY 421 SerGlySerSerGluSerAspGlyAsp 430
Db 1498 AGTGGCAGTTCAGAGTGAAGCGATGGTGAC 1527
```

RESULT 4

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US-09-794-422-45
; Sequence 45, Application US/09794422
; Publication No. US20030166239A1
; GENERAL INFORMATION:
; APPLICANT: Brown, Thomas A.
; APPLICANT: De Wet, Jeffrey R.
; APPLICANT: Gowen, Lori C.
; APPLICANT: Hames, Lynn M.
; TITLE OF INVENTION: Mammalian Osteoregulins
; FILE REFERENCE: PCI0445
; CURRENT APPLICATION NUMBER: US/09/794,422
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 60/185,617
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 60/234,500
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45
; LENGTH: 1969
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-794-422-45
```

```
Alignment Scores:
Pred. No.: 2,96e-213 Length: 1969
Score: 2276.00 Matches: 429
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.77% Mismatches: 0
Query Match: 99.87% Indels: 0
DB: 12 Gaps: 0
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US-09-700-696C-2 (1-430) x US-09-794-422-45 (1-1969)

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QY 1 ValAsnLysGluTyrSerIleSerAsnLysGluAsnThrHisAsnGlyLeuArgMetSer 20
Db 331 CTGATAAAGAAATATAGTATCAGTAACAAAGAGAAATACTCACATGGCTCAGGATGTCA 390
QY 21 IleTyrProLysSerThrGlyAsnLysGlyPheGluAspGlyAspAlaIleSerLys 40
Db 391 ATTATTCCTTAAGTCACTGGGAATAAAGGTTTGAAGATGGAGATGATGCTATCAGCAA 450
QY 41 LeuHisAspGlnGluTyrGlyAlaAlaLeuIleArgAsnAsnMetGlnHisIleMet 60
Db 451 CTACATGACCAAGAGAAATATGGCGAGCTCTCATCAGAAATAACATGCAACATATAATG 510
QY 61 GlyProValThrAlaIleLysLeuLeuGlyGluGluAsnLysGluAsnThrProArgAsn 80
Db 511 GGCCCACTGACTCGGATTAACACTCTCTGGGGAAAGAAACAAAGAGAACACACCTAGGA 570
QY 81 ValLeuAsnIleIleProAlaSerMetAsnTyrAlaLysAlaHisSerLysAspLysLys 100
Db 571 GTTCTAAACATATCCAGCAGTATGAATATGCTTAAGCACACTCGAAGGATAAAAG 630
QY 101 LysProGlnArgAspSerGlnAlaGlnLysSerProValLysSerLysSerThrHisArg 120
Db 631 AAGCCTCAAGAGATTCCTCAAGCCAGAAAAGTCCAGTAAAAAGCAAAACACCCATCGT 690
QY 121 IleGlnHisAsnIleAspTyrLeuLysHisLeuSerLysValLysLysIleProSerAsp 140
Db 691 ATTCAACAACAACATTCACCTACCTAAACACATCTCTCAAAAGTCAAAAATAATCCCCAG 750
QY 141 PheGluGlySerGlyTyrThrAspLeuGlnGluArgGlyAspAsnAspIleSerProPhe 160
Db 751 TTTGAAGGACGCGTTATACAGATCTTCAAGAGAGAGGGACAAATGATATATCTCTTTTC 810
QY 161 SerGlyAspGlyGlnProPheLysAspIleProGlyLysGlyGluAlaThrGlyProAsp 180
Db 811 AGTGGGACGCGCAACCTTTTAAGGACATTCCTGGTAAAGGAGAGACTACTGTCTCTGAC 870
QY 181 LeuGluGlyLysAspIleGlnThrGlyPheAlaGlyProSerGluAlaGluSerThrHis 200
Db 871 CTAGAGGCAAAAGATATTCAACAGGGTTTGCAGGCCCCAAGTGAAGCTGAGAGTACTCAT 930
QY 201 LeuAspThrLysLysProGlyTyrAsnGluIleProGluArgGluGluAsnGlyGlyAsn 220
Db 931 CTTGACACAAAAAGCCAGGTATATAATGAGATCCCAAGAGAGAGAGAAATGGTGAAT 990
QY 221 ThrIleGlyThrArgAspGluThrAlaLysGluAlaAspAlaValSerLeuVal 240
Db 991 ACCATTGGAACCTAGGATGAAACTCGAAAGAGGCGAGATGCTGTTGATGCTCAGCCCTTGA 1050
QY 241 GluGlySerAsnAspIleMetGlySerThrAsnPhelLysGluLeuProGlyArgGluGly 260
Db 1051 GAGGCGACGACGATATCATGGGTAGTACCAATTTTAAGGAGCTCCCTGGAGAGAGGA 1110
QY 261 AsnArgValAspAlaGlySerGlnAsnAlaHisGlnGlyLysValGluPheHisTyrPro 280
Db 1111 AACAGAGTGTGCTGGCAGCCAAATGCTCACCAAGGGAAGGTGTGATTTTCATTACCT 1170
QY 281 ProAlaProSerLysGluLysArgLysGluGlySerSerAspAlaAlaGluSerThrAsn 300
Db 1171 CCTGCACCTCTCAAAAGAGAGAAAGAAAGAGGCGAGTGTGATGCTGAGCTGAAGTACCAAC 1230
QY 301 TyrAsnGluIleProLysAsnGlyLysGlySerThrArgLysGlyValAspHisSerAsn 320
Db 1231 TATAATGAATTCCTAAAAATGGCAAGGCGAGTACCAGAAAGGGTGTAGATCATTTCTAAT 1290
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QY 321 ArgAsnGlnAlaThrLeuAsnGluLysGlnArgPheProSerLysGlyLysSerGlnGly 340
Db 1291 AGGAACCAAGCAACCTTAAATGAAAAACAAAGGTTTCTAGTAAGGCAAAAGTCAGGCG 1350
QY 341 LeuProIleProSerArgGlyLeuAspAsnGluLysAsnGluMetAspSerPheAsn 360
Db 1351 CTGCCCATTCCTCTCTGCTGCTTGAATGAATCAAAACGAAATGGATTCCTTTAAT 1410
QY 361 GlyProSerHisGluAsnIleIleThrHisGlyArgLysTyrHisTyrValProHisArg 380
Db 1411 GGCCCCAGTCATGAGAAATAATAACACATGGCAGAAAAATATCATATGTACCCACAGA 1470
QY 381 GlnAsnSerThrArgAsnLysGlyMetProGlnLysGlySerTrpGlyArgGln 400
Db 1471 CAAAAATAATTCACAGGAATAAGGGTATGCCCAAGGGAAAGGCTCTCGGGGTAGACAA 1530
QY 401 ProHisSerAsnArgPheSerSerArgArgAspAspSerSerGluSerSerAsp 420
Db 1531 CCCCATTCACACAGGAGGTTTACTTCCCGTAGAAGGATGACAGTAGTGTATCTGAC 1590
QY 421 SerGlySerSerGluSerAspGlyAsp 430
Db 1591 AGTGGCAGTTCAAGTGAGAGCGATGGTGAC 1620

RESULT 5
US-09-794-422-5
; Sequence 5, Application US/09794422
; Publication No. US20030166239A1
; GENERAL INFORMATION:
; APPLICANT: Brown, Thomas A.
; APPLICANT: De Wet, Jeffrey R.
; APPLICANT: Gowen, Lori C.
; APPLICANT: Hames, Lynn M.
; TITLE OF INVENTION: Mammalian Osteoregulins
; FILE REFERENCE: PC10445
; CURRENT APPLICATION NUMBER: US/09/794,422
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 60/185,617
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 60/234,500
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 2019
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-794-422-5

Alignment Scores:
Pred. No.: 3,06e-213 Length: 2019
Score: 2276.00 Matches: 429
Percent Similarity: 100.00% Conservative: 1
Best local Similarity: 99.77% Mismatches: 0
Query Match: 99.87% Indels: 0
DB: 12 Gaps: 0

US-09-700-696C-2 (1-430) x US-09-794-422-5 (1-2019)

QY 1 ValAsnLysGluTyrSerIleSerAsnLysGluAsnThrHisAsnGlyLeuArgMetSer 20
Db 381 CTGAATAAAGATATAGTATCATCAACAAAGAGATACTCAACATGGCCCTGAGGATGTCA 440
QY 21 IleTyrProLysSerThrGlyAsnLysGlyPheGluAspGlyAspAlaIleSerLys 40
Db 441 ATTTATCTCACTCACTGGAATAAAGGGTTTGAAGATGGAGATCATCTATCAGCAAA 500
QY 41 LeuHisAspGlnGluTyrGlyValAlaLeuIleArgAsnMetGlnHisIleMet 60
Db 501 CTACATGACCAAGAAAGATATGGCGCAGCTCTCATCAGAAATAAATGCAACATATAATG 560
QY 61 GlyProValThrAlaIleLysLeuLeuGlyGluGluAsnLysGluAsnThrProArgAsn 80
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Db 561 GGCCCACTGACTCGGATTAAACTCTCTGGGGGAGAAACAAAGAGAACACACCTTAGGAAT 620
QY 81 ValLeuAsnIleIleProAlaSerMetAsnTyrAlaLysAlaHisSerLysAspLysLys 100
Db 621 GTTCTAAACATATATCCAGCAAGTATGAATATGCTTAAGCACACTCGAAGGATAAAAG 680
QY 101 LysProGlnArgAspSerGlnAlaGlnLysSerProValLysSerLysSerThrHisArg 120
Db 681 AAGCCTCAAGAGATTCCTCAAGCCAGAAAAGTCCAGTAAAAAGCAAAAGCACCCTCGT 740
QY 121 IleGlnHisAsnIleAspTyrLeuLysHisLeuSerLysValLysLysIleProSerAsp 140
Db 741 ATTCAACACACAACTGACTACCTTAAACCATCTCTCAAAAGTCAAAAAAATCCCCAGTAT 800
QY 141 PheGluGlySerGlyTyrThrAspLeuGlnGluArgGlyAspAsnAspIleSerProPhe 160
Db 801 TTTGAAGGCGAGCGTTATACAGATCTTCAAGAGAGAGGGGACATGATATATCTCTCTTC 860
QY 161 SerGlyAspGlyGlnProPheLysAspIleProGlyLysGlyGluAlaThrGlyProAsp 180
Db 861 AGTGGGCGAGCGCAACCTTTTAAAGGACATTCCTGGTAAAGGAGAGCTACTGGTCTTGAC 920
QY 181 LeuGluGlyLysAspIleGlnThrGlyPheAlaGlyProSerGluAlaGluSerThrHis 200
Db 921 CTAGAAGGCGAAGATATTCAACAGGGTTTGCAGGGCCCAAGTGAAGCTGAGAGTACTCAT 980
QY 201 LeuAspThrLysLysProGlyTyrAsnGluIleProGluArgGluGluAsnGlyGlyAsn 220
Db 981 CTTGACACAAAAAGCCAGGTTATATGAGATCCACAGAGAGAGAGAAATGTTGGAAAT 1040
QY 221 ThrIleGlyThrArgAspGluThrAlaLysGluAlaAspAlaValAspValSerLeuVal 240
Db 1041 ACCATTGGAACTAGGATGAACTGCGAAAGAGGAGAGATGCTGTGTATGTGACCTTGTA 1100
QY 241 GluGlySerAsnAspIleMetGlySerThrAsnPheLysGluLeuProGlyArgGluGly 260
Db 1101 GAGGGCAGCAACGATATCATGGGTAGTACCAATTTTAAAGGAGCTCCCTGGAAGAAGGA 1160
QY 261 AsnArgValAspAlaGlySerGlnAsnAlaHisGlnGlyValGluPheHisTyrPro 280
Db 1161 AACAGATGGATGCTGGCAGCCAAAATGCTCACCAAGGGAAGGTTGAGTTTCAATCCCT 1220
QY 281 ProAlaProSerLysGluLysArgLysGluGlySerSerAspAlaAlaGluSerThrAsn 300
Db 1221 CCTGCACCTCAAAAGAGAAAGAAAGAGGAGGAGTGTGATGACAGCTGAAAGTACCAAC 1280
QY 301 TyrAsnGluIleProLysAsnGlyLysGlySerThrArgLysGlyValAspHisSerAsn 320
Db 1281 TATAATGAAATTCCTAAAAATGGCAAGGAGTACCAGAAAGGCTGTAGATCATCTTAAT 1340
QY 321 ArgAsnGlnAlaThrLeuAsnGluLysGlnArgPheProSerLysGlyLysSerGlnGly 340
Db 1341 AGGAACCAAGCAACCTTAAATGAAAAACAAAGTTCCTAGTAAGGCAAAAGTCAGGCG 1400
QY 341 LeuProIleProSerArgGlyLeuAspAsnGluLysAsnGluMetAspSerPheAsn 360
Db 1401 CTGCCCATTCCTCTCTGCTGTGATAATGAATCAAAACGAAATGGATTCCTTTAAT 1460
QY 361 GlyProSerHisGluAsnIleIleThrHisGlyArgLysTyrHisTyrValProHisArg 380
Db 1461 GGCCCCAGTCATGAGAAATAATAACACATGGCAGAAAAATATCATATGTACCCACAGA 1520
QY 381 GlnAsnSerThrArgAsnLysGlyMetProGlnGlyLysGlySerTrpGlyArgGln 400
Db 1521 CAAATATATTCACAGGAATAAGGGTATGCCCAAGGGAAAGGCTCTCTGGGGTAGACAA 1580
QY 401 ProHisSerAsnArgPheSerSerArgArgAspAspSerSerGluSerSerAsp 420
Db 1581 CCCCATTCCACAGGAGGTTTAGTTCCCGTAGAAGGATGACAGTAGTAGTCACTCTGAC 1640
QY 421 SerGlySerSerGluSerAspGlyAsp 430
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| | | | |
|---|------|--|------|
| Db | 1641 | AGTGGCAGTTCAAGTGAGCGATGGTGAC | 1670 |
| RESULT 6 | | | |
| US-09-794-422-7 | | | |
| ; Sequence 7, Application US/09794422 | | | |
| ; Publication No. US20030166239A1 | | | |
| ; GENERAL INFORMATION: | | | |
| ; APPLICANT: Brown, Thomas A. | | | |
| ; APPLICANT: De Wet, Jeffrey R. | | | |
| ; APPLICANT: Gowen, Lori C. | | | |
| ; APPLICANT: Hames, Lynn M. | | | |
| ; TITLE OF INVENTION: Mammalian Osteoregulins | | | |
| ; FILE REFERENCE: PC10445 | | | |
| ; CURRENT APPLICATION NUMBER: US/09/794,422 | | | |
| ; CURRENT FILING DATE: 2001-02-27 | | | |
| ; PRIOR APPLICATION NUMBER: 60/185,617 | | | |
| ; PRIOR FILING DATE: 2000-02-29 | | | |
| ; PRIOR APPLICATION NUMBER: 60/234,500 | | | |
| ; PRIOR FILING DATE: 2000-09-22 | | | |
| ; NUMBER OF SEQ ID NOS: 46 | | | |
| ; SOFTWARE: PatentIn Ver. 2.0 | | | |
| ; SEQ ID NO 7 | | | |
| ; LENGTH: 2112 | | | |
| ; TYPE: DNA | | | |
| ; ORGANISM: Homo sapiens | | | |
| US-09-794-422-7 | | | |
| Alignment Scores: | | | |
| Pred. No.: 3,25e-213 Length: 2112 | | | |
| Score: 2276.00 Matches: 429 | | | |
| Percent Similarity: 100.00% Conservative: 1 | | | |
| Best Local Similarity: 99.77% Mismatches: 0 | | | |
| Query Match: 99.87% Indels: 0 | | | |
| DB: 12 Gaps: 0 | | | |
| US-09-700-696c-2 (1-430) x US-09-794-422-7 (1-2112) | | | |
| QY | 1 | ValAsnLysGluTyrSerIleSerLysLysGluAsnThrHisAsnGlyLeuArgMetSer | 20 |
| Db | 474 | CTGAATAAGAAATATAGTATCATGTAACAAAGAGAAATCTCATATGGCTGAGGATGTCA | 533 |
| QY | 21 | IleTyrProLysSerThrGlyAsnLysGlyPheGluAspGlyAspAspAlaIleSerLys | 40 |
| Db | 534 | ATTATCTCACTAAGTCACTGGAATAAAGGTTTGAGGATGGAGATGATGCTATCAGCAA | 593 |
| QY | 41 | LeuHisAspGluGluTyrGlyAlaIleAlaIleArgAsnAsnMetGluHisIleMet | 60 |
| Db | 594 | CTACATGACCAAGAAAGATATGCGCAGCTCTCATCAGAAATAACATGCAACATATAATG | 653 |
| QY | 61 | GlyProValThrAlaIleLysLeuLeuGlyGluAsnLysGluAsnThrProArgAsn | 80 |
| Db | 654 | GGGCCAGTGACTCGGATTAACTCTGGGGGAAGAAACAAAGAGAACACACACCTAGGAAT | 713 |
| QY | 81 | ValLeuAsnIleIleProAsnSerMetAsnTyrAlaLysAlaHisSerLysAspLysLys | 100 |
| Db | 714 | GTCTAAACATATATCCCAAGATATGATTAATGCTAAAGCACATCGAAGGATAAAAG | 773 |
| QY | 101 | LysProGlnArgAspSerGlnAlaGlnLysSerProValLysSerLysSerThrHisArg | 120 |
| Db | 774 | AGGCTCAAGAGATTCACAGCCAGCAAAAGTCCAGTAAAGCAAAAGCACCCATCGT | 833 |
| QY | 121 | IleGlnHisAsnIleAspTyrLysLysHisLeuSerLysValLysLysIleProSerAsp | 140 |
| Db | 834 | ATTCAACACAACTTACTACCTAAACATCTCTCAAAAGTCAAAATAATCCCAAGTAT | 893 |
| QY | 141 | PheGluGlySerGlyTyrThrAspLeuGlnArgGlyAspAsnAspIleSerProPhe | 160 |
| Db | 894 | TTTGAAGGAGCGGTTTATACAGATCTTCAAGAGAGAGGAGCAATATATCTCTCTTC | 953 |
| QY | 161 | SerGlyAspGlyGlnProPheLysAspIleProGlyLysGlyGluAlaThrGlyProAsp | 180 |
| Db | 954 | AGTGGGCGCGCCCACTTTTAAAGGACATCTCTGTTAAAGGAGAGAGTACTGCTCTGAC | 1013 |
| QY | 181 | LeuGluGlyLysAspIleGlnThrGlyPheAlaGlyProSerGluAlaGluSerThrHis | 200 |
| Db | 1014 | CTAGAAGGCAAGAATATTCAACAGGGTTTGAGGCCCCCAAGTGAAGCTGAGAGTACTCAT | 1073 |
| QY | 201 | LeuAspThrLysLysProGlyTyrAsnGluIleProGluArgGluGluAsnGlyGlyAsn | 220 |
| Db | 1074 | CTTGACACAAAAAGCCAGGTTTATATGAGATCCCAAGAGAGAGAAATGGTGGAAT | 1133 |
| QY | 221 | ThrIleGlyThrArgAspGluThrAlaLysGluAlaAspAlaValAspValSerLeuVal | 240 |
| Db | 1134 | ACCATTTGGAACTAGGGATGAATCTCGGAAGAGGAGAGATGCTGTTGATGTGAGCTTGT | 1193 |
| QY | 241 | GluGlySerAsnAspIleMetGlySerThrAsnLysGluLeuProGlyArgGluGly | 260 |
| Db | 1194 | GAGGGCAGCAACGATATCATGCTGTTTAAAGGAGCTCCCTGGAGAGAGAGGA | 1253 |
| QY | 261 | AsnArgValAspAlaGlySerGlnAsnAlaHisGlnGlyLysValGluPheHisTyrPro | 280 |
| Db | 1254 | AACAGATGGATGCTGGCAGCCAAATGCTCAAGGAGAGGTTGAGTTTCATTACCT | 1313 |
| QY | 281 | ProAlaProSerLysGluLysArgLysGluGlySerSerAspAlaAlaGluSerThrAsn | 300 |
| Db | 1314 | CCTGCACCTCAAAAGAGAGAAAGAGAGGAGCTAGTGCAGCTGAAAGTACCAAC | 1373 |
| QY | 301 | TyrAsnGluIleProLysAsnGlyLysGlySerThrArgLysGlyValAspHisSerAsn | 320 |
| Db | 1374 | TATAATGAATTTCTTAAATGCAAGGAGCTACCAAGAGGAGGTTAGATCATTTCTAAT | 1433 |
| QY | 321 | ArgAsnGlnAlaThrLeuAsnGluLysGlnArgPheProSerLysGlyLysSerGlnGly | 340 |
| Db | 1434 | AGGAACCAAGCAACCTTAAATGAAAAACAAAGTTTCTTAGTAAGGCAAAAGTCAGGC | 1493 |
| QY | 341 | LeuProIleProSerArgGlyLeuAspAsnGluIleLysAsnGluMetAspSerPheAsn | 360 |
| Db | 1494 | CTGCCCATTCCTCTCTGCTGTTGATAATGAATCAAAAGCAAAAGTATGATTCCTTAAT | 1553 |
| QY | 361 | GlyProSerHisGluAsnIleIleThrHisGlyArgLysTyrHisTyrValProHisArg | 380 |
| Db | 1554 | GGCCCCAGTCAGAGATATATAACACATGGCAGAGAAATATCATTTATGTACCCACAGA | 1613 |
| QY | 381 | GlnAsnAsnSerThrArgAsnLysGlyMetProGlnGlyLysGlySerTrpGlyArgGln | 400 |
| Db | 1614 | CAAAATAATTTACACGGAATAGGGTATGCCCAAGAGGAAAGGCTCTCTGGGGTAGACAA | 1673 |
| QY | 401 | ProHisSerAsnArgPheSerSerArgArgArgAspAspSerGluSerSerAsp | 420 |
| Db | 1674 | CCCATTCCAACAGGAGGTTTATGTTCCCGTAGAGGAGTACAGTAGTAGTGTGATCTGAC | 1733 |
| QY | 421 | SerGlySerSerSerGluSerAspGlyAsp | 430 |
| Db | 1734 | AGTGGCAGTTTCAAGTGAGAGCGATGCTGAC | 1763 |
| RESULT 7 | | | |
| US-09-794-422-3 | | | |
| ; Sequence 3, Application US/09794422 | | | |
| ; Publication No. US20030166239A1 | | | |
| ; GENERAL INFORMATION: | | | |
| ; APPLICANT: Brown, Thomas A. | | | |
| ; APPLICANT: De Wet, Jeffrey R. | | | |
| ; APPLICANT: Gowen, Lori C. | | | |
| ; APPLICANT: Hames, Lynn M. | | | |
| ; TITLE OF INVENTION: Mammalian Osteoregulins | | | |
| ; FILE REFERENCE: PC10445 | | | |
| ; CURRENT APPLICATION NUMBER: US/09/794,422 | | | |
| ; CURRENT FILING DATE: 2001-02-27 | | | |
| ; PRIOR APPLICATION NUMBER: 60/185,617 | | | |
| ; PRIOR FILING DATE: 2000-02-29 | | | |
| ; PRIOR APPLICATION NUMBER: 60/234,500 | | | |
| ; PRIOR FILING DATE: 2000-09-22 | | | |
| ; NUMBER OF SEQ ID NOS: 46 | | | |
| ; SOFTWARE: PatentIn Ver. 2.0 | | | |
| ; SEQ ID NO 3 | | | |
| ; LENGTH: 1682 | | | |


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QY 144 rGlyTyrThrAspLeuGlnGluArgGlyAspAsnAspIleSerProPheSerGlyAspG1 164
Db 5664 AGAAGATGATGACAGTCATGACATCAGACACTAATAATAGTGACAGTAAATGCCAATGG 5723
QY 164 yGlnProPheLysAsp-----IleProGlyLysGlyGluAlaThrGlyPr 179
Db 5724 TAACAATGGGAATGATGACAATGACAAATCAGACAGTGGCAAGGTAAATCAGATACGAG 5783
QY 179 oAspLeuGluGlyLysAspIleGlnThrGlyPheAlaGlyProSerGluAlaGluSerTh 199
Db 5784 TGACAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5843
QY 199 rHisLeuAspThrLysLysProGlyTyrAsnGluIleProGluArgGluGluAsnGlyG1 219
Db 5844 CAGCAGTATGACAAACAGTACAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 5903
QY 219 yAsnThrIleGlyThrArgAspGluThrAlaLysGluAlaAspAlaValAspValSerLe 239
Db 5904 CAGTGACAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5960
QY 239 uValGluGlySerAsnAspIleMetGlySerThrAsnPhelLysGluLeuProGlyArg-- 258
Db 5961 TAGCAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6020
QY 259 -----GluGlyAsnArgValAspAlaGlySerGlnAsnAlaHisGlnGlyLysValG1 276
Db 6021 AGNAGCGCAGCAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6080
QY 276 uPheHisTyrProProAlaProSerLysGluLysArgLysGluGlySerSerAspAla1 296
Db 6081 CAGTAGTGACAAACAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 6140
QY 296 aGluSerThrAsnTyrAsnGluIleProLysAsnGlyLysGlySerThrArgLysGlyVa 316
Db 6141 TGACAGCAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 6195
QY 316 lAspHisSerAsnArgAsnGlnAlaThrLeuAsnGluLysGlnArgPheProSerLysG1 336
Db 6196 -GACAGCAGCAGCAGCAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 6254
QY 336 yLysSerGlnGlyLeuProIleProSerArgGlyLeuAspAsnGluIleLysAsnGluMe 356
Db 6255 CAGTGATAGT-----AGTGACAGCAGTATGATGATGATGATGATGATGATGATGATGATG 6299
QY 356 tAspSerPheAsnGlyProSerHisGluAsnIleThrHisGlyArgLysTyrHisTy 376
Db 6300 TGACAGCAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 6330
QY 376 rValProHisArgGlnAsnSerThrArgAsnLysGlyMetProGlnGlyLysGlySe 396
Db 6331 -----GACAGCAGCAACAGCAGCAGTATGATGATGATGATGATGATGATGATGATGATG 6380
QY 396 rTrpGlyArgGlnProHisSerAsnArgArgPheSerSerArgArgAsp-----413
Db 6381 CAGCAACAGCAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 6440
QY 414 -----AspSerSerGluSerSerAspSerGlySerSerSerGluSerSerGluSerAsp 428
Db 6441 TAGCAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6492
```

RESULT 10

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US-09-785-770A-15
; Sequence 15, Application US/09785770A
; Patent No. US20020103360A1
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: A NOVEL PROTEIN RELATED TO MELANOMA-INHIBITING PROTEIN
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 07334-328001
; CURRENT APPLICATION NUMBER: US/09/785, 770A
; CURRENT FILING DATE: 2001-02-16
```

```
; PRIOR APPLICATION NUMBER: US 09/387,462
; PRIOR FILING DATE: 1999-09-01
; PRIOR APPLICATION NUMBER: US 09/145,056
; PRIOR FILING DATE: 1998-09-01
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 4.0
; SEQ ID NO 15
; LENGTH: 5721
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)....(5721)
US-09-785-770A-15

Alignment Scores:
Pred. No.: 0.000382 Length: 5721
Score: 148.00 Matches: 106
Percent Similarity: 34.76% Conservatives: 65
Best Local Similarity: 21.54% Mismatches: 209
Query Match: 6.49% Indels: 112
DB: 10 Gaps: 24

US-09-700-696C-2 (1-430) x US-09-785-770A-15 (1-5721)
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```
QY 1 ValAsnLysGluTyrSerIleSerAsnLys-----GluAsnThrHisAsnGly 16
Db 1372 GTAACGCGCAGAACATCACATTAAGGAAAGGAGGGAGGTTCAGGAATCCAAGAGGGGC 1431
QY 17 Leu-----ArgMetSerIleTyrPro 23
Db 1432 CTGGTACAGATGAGCAGAAATTAGAGGATGAAATCAAGAGGCATGACTGTGCACAGT 1491
QY 24 LysSerThrGlyAsnLys-----GlyPheGluAspGlyAspAlaIle 38
Db 1492 TCTGTTTCACAGCAATACCTCACTCTATGCCAGCTGCTGAAAGGGTAAAGACACATTA 1551
QY 39 SerLysLeuHisAspGlnGlu-----TyrGlyAlaAlaLeu-----IleArgAsn 54
Db 1552 AAATCAGCTTATGATGATACAGAAATGACCTAAAGAGGAGCAGCTATTATCTCAAAA 1611
QY 55 AsnMetGlnHisIleMetGlyProValThrAlaIleLysLeuLeuGlyGluGluAsnLys 74
Db 1612 GGAATGCTCCAGAAAGAAAGCCTGAGAGCAGATTTTGGAAAGTGGCTCAGAGAGTGAA 1671
QY 75 -----GluAsnThrProArgAsnValLeuAsn-----IleIleProAlaSerMet 89
Db 1672 TCTGCACAGAAAGCTGCAGGGAATCAATGAATGACAGAAAGATTCAACAGGAATCCCTG 1731
QY 90 AsnTyrAlaLysAlaHisSerLysAspLysLysLysProGlnArgAspSerGlnAlaGln 109
Db 1732 GGTAGTGACACCACTCATGGGAGATGACCACCTAACGCATCCAGACAGAGTGTGGAGGA 1791
QY 110 LysSerProValLysSerLysSerThrHis-----ArgIleGlnHisAsnIleAspTyr 127
Db 1792 GACGCTTGGTAAATGGGGCCAAACCTGCACACGCTTTTCAGTGGAGCATCAACGTGAGGA 1851
QY 128 LeuLysHis-----LeuSerLysValLysLysIleProSerAspPheGluGlySerGly 145
Db 1852 TTGAAAGAGGAATTAGTTCTTAAACTCAAAACCAACCTAGA---TTCCTCTCTCCAGAT 1908
QY 146 TyrThrAspLeuGlnGluArgGlyAspAsnAspIleSerProPheSerGlyAspGlyGln 165
Db 1909 GAGATTGATTATGCCAGAGAACTGGAAGACGAGGT---CCCATTTCTGGAGAAATCTT 1965
QY 166 ProPhe-----LysAspIleProGlyLysGlyAlaThrGlyProAspLeuGlu 182
Db 1966 CCTCGCAACAAAGAAAGAGATGTG-----GCTGCCACAGCCAGCAAGCAAAATG 2013
QY 183 GlyLysAspIleGlnThrGlyPheAlaGlyProSerGluAlaGluSerThrHisLeuAsp 202
Db 2014 ACTGAGAGATAGG-----CTCTCTGAGGAGAGCAAGCAAGAGAGCATCTCTGGAT 2064
```

```

QY 203 ThrLysLysProGlyTyrAsnGluLeuProGluArgGluGluAsnGlyGlyAsnThrIle 222
Db 2065 -----GAAGAGT-----CATCACAAGGCAATGCAGGGCAGACAGAGTA 2106
QY 223 GlyThrArgAspGluThr-----AlaLysGlu 231
Db 2107 GGACAGACAGACCAAACTGACACAGCAGGAGCAGCTTCCCTTCTAAAGTAGAGAG 2166
QY 232 AlaAspAlaValSerLeuValGluGlySerAsnIleMetGlySerThrAsn 251
Db 2167 GATGATTATCCCTCTGAAGAACTACTAGAGATGAAACCGTATAAATGCAAAACGGTCT 2226
QY 252 PheLysGluLeuProGlyArgGluGlyAsnArgValAspAlaGlySerGln----- 268
Db 2227 AAGAAAAAACCCGGGAATCAGCGCAGGAGCTTTGATGTAATCTGCAAGTCCCTGAC 2286
QY 269 AsnAlaHisGlnGlyLysValGluPheHisTyrProProAlaProSerLysGluLysArg 288
Db 2287 AGAGCAGT-----TAGGACCAATTCAT-----CCAGATCCAGAAATTTGAAGAAAGC 2334
QY 289 LysGluGlySerSerAspAlaAlaGluSerThrAsnTyrAsnGluLeuProLysAsnGly 308
Db 2335 AAGCAAGAACTAGTATGATTTTCGATAGTGAATAAAGCAAGTGAG----- 2379
QY 309 LysGlySerThrArgLysGlyValAspHisSerAsnArgAsnGlnAlaThrLeuAsnGlu 328
Db 2380 -----ACTGCTGCCAAAGGGTCAACACAGGAGCGAGGAAACAAAGTGAG----- 2433
QY 329 LysGlnArg-----PheProSerLysGlyLysSer 338
Db 2434 AAAGACGCCCTCTGGCAGATAGAAAGACACAGAGACCATTTGAACGAAAGTGACTTTCT 2493
QY 339 GlnGlyLeuProLysProSerArgGlyLeuAspAsnGluLeuLysAsnGluMetAspSer 358
Db 2494 GACAGCAATAAAATTCAGACTCCAGATAGTGAAGTGTTCAGATAAAGATTCGTAT 2553
QY 359 Phe-----AsnGlyProSerHisGluAsnIleThrHisGlyArgLysTyrHisTyr 376
Db 2554 TATCTGAAGAACGACCAACCTCGAGGAACATCTGAAGACCTCAGGCTT----- 2601
QY 377 ValProHisArgGlnAsnAsnSerThrArgAsnLysGlyMetProGlnGlyLysGlySer 396
Db 2602 -----GCAGGGAGCGCTGAGGAGAACTCTCA 2628
QY 397 TrpGlyArgGlnProHisSerAsnArgArgPheSerSerArgArgAspAspSerSer 416
Db 2629 -----AAAGAGACCAATGAGAAC-----ACAGAGAAGTACATGGGCACA 2667
QY 417 GluSerSerAspSerGlySerSerSerGluSerAsp 428
Db 2668 GAAAGCCAGGGGCTGCTGCTGCAGAACCTGAAGAT 2703

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RESULT 11

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US-09-785-770A-14
; Sequence 14, Application US/09785770A
; Patent No. US20020103360A1
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; APPLICANT: Barnes, Thomas M.
; TITLE OF INVENTION: A NOVEL PROTEIN RELATED TO MELANOMA-INHIBITING PROTEIN
; FILE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 07334-328001
; CURRENT FILING DATE: 2001-02-16
; CURRENT APPLICATION NUMBER: US/09/785,770A
; PRIOR APPLICATION NUMBER: US 09/387,462
; PRIOR FILING DATE: 1999-09-01
; PRIOR APPLICATION NUMBER: US 09/145,056
; PRIOR FILING DATE: 1998-09-01
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 4.0
; SEQ ID NO 14
; LENGTH: 8121
; TYPE: DNA

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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: (1)...(4)
; NAME/KEY: CDS
; LOCATION: (5)...(5725)
; NAME/KEY: 3'UTR
; LOCATION: (5726)...(8121)
US-09-785-770A-14
Alignment Scores:
Pred. No.: 0.000603 Length: 8121
Score: 148.00 Matches: 106
Percent Similarity: 34.76% Conservative: 65
Best Local Similarity: 21.54% Mismatches: 209
Query Match: 6.49% Indels: 112
DB: 10 Gaps: 24
US-09-700-696C-2 (1-430) x US-09-785-770A-14 (1-8121)
QY 1 ValAsnLysGluTyrSerIleSerAsnLys-----GluAsnThrHisAsnGly 16
Db 1376 GTAAACGACGACATCATTTAAAGAAAGGGAGGGAGTTTCAGGATCCAAAGGGGC 1435
QY 17 Leu-----ArgMetSerIleTyrPro 23
Db 1436 CTGGTACAGATGAGACAGAAATTAGAGATCAAAATCAAGAAGGCATGACTGTGCACAGT 1495
QY 24 LysSerThrGlyAsnLys-----GlyPheGluAspGlyAspAspAlaIle 38
Db 1496 TCTGTTTCAGACGATAACCTCAACTCTATGCCAGCTCTGAAAAGGGTAAAGACACATTA 1555
QY 39 SerLysLeuHisAspGlnGlu-----TyrGlyAlaAlaLeu-----IleArgAsn 54
Db 1556 AAATCAGCTTATGATGATACAGAAATGACCTAAAGAGGAGCAGCTATTCTATCTCAAAA 1615
QY 55 AsnMetGlnHisIleMetGlyProValThrAlaIleLysLeuLeuGlyGluAsnLys 74
Db 1616 GGAATGCTCCAGCAAGAAAGCCCTGGAGAGCAGATTTTGAAGGTGGCTCAGAGAGTGAA 1675
QY 75 -----GluAsnThrProArgAsnValLeuAsn-----IleIleProAlaSerMet 89
Db 1676 TCTGCACAGAAAGCTGAGGGAATCAATGAATGACAGAAAGATTCAACAGGAATCCCTGT 1735
QY 90 AsnTyrAlaLysAlaHisSerLysAspLysLysLysProGlnArgAspSerGlnAlaGln 109
Db 1736 GGTAGTGCACCACTCTATGGGAGATGACCACCTAACGCATCCACAGACAGTGTGGAGGA 1795
QY 110 LysSerProValLysSerLysSerThrHis-----ArgIleGlnHisAsnIleAspTyr 127
Db 1796 GACGCTTTGGTAAATGGGGCCAAACTGCACACGCTTTTCAGTGGAGCATCAACGTGAGAA 1855
QY 128 LeuLysHis-----LeuSerLysValLysLysIleProSerAspPheGluGlySerGly 145
Db 1856 TTGAAGAGGAATAGTTCTTAAACTCAAAACCACTAGA---TTCTCCTCTCCAGAT 1912
QY 146 TyrThrAspLeuGlnGluArgGlyAspAsnAspIleSerProPheSerGlyAspGlyGln 165
Db 1913 GAGATTGATTGGCCAGAGAACTGGAGAGCAGAGTT---CCCATTCTGGGAAGAAATCTTT 1969
QY 166 ProPhe-----LysAspIleProGlyLysGlyGluAlaThrGlyProAspLeuGlu 182
Db 1970 CCTGGCAACAAGAAAGAGATGTG-----GCTGCCACGACGAGTAAGCAAAATG 2017
QY 183 GlyLysAspIleGlnThrGlyPheAlaGlyProSerGluAlaGluSerThrHisLeuAsp 202
Db 2018 AGTGAAAGATTAAG-----CTCTCTGAGGAGAGCAACCAAGAGGACTCTCTTGAT 2068
QY 203 ThrLysLysProGlyTyrAsnGluLeuProGluArgGluGluAsnGlyGlyAsnThrIle 222
Db 2069 -----GAAGAGT-----CATCACAAGGCAATGCAGGGCAGACAGAGTA 2110
QY 223 GlyThrArgAspGluThr-----AlaLysGlu 231

```

```

Db      2111  GGCACAGACACCAAACTGCACACAGGAGCCAGCTTCCTTTCTAAAGTAGAGAG 2170
              |||:::||||
QY      232  AlaAspAlaValAspValSerLeuValGluGlySerAsnAspMetGlySerThrAsn 251
              |||:::||||
Db      2171  GATGATTATCCTCTGAGAACTACTAGAGGATGAAACGCTATAAATGCAAAACGGTCT 2230
              |||:::||||
QY      252  PheGlyLeuProGlyArgGlyAsnArgValAspAlaGlySerGln----- 268
              :::::|||||
Db      2231  AAGAAAAAACCGGGAATCAGGCGAGCTTTGATGTTTAAATCTGCAAGTCCCTGAC 2290
              :::::|||||
QY      269  AsnAlaHisGlnGlyValAspPheHisTyProProAlaProSerLysGluLysArg 288
              |||:::||||
Db      2291  AGAGCAGTTTATAGGACCAATCAT-----CCAGATCCAGAAATTGAGAAAGC 2338
              |||:::||||
QY      289  LysGluGlySerSerAspAlaAlaGluSerThrAsnTyrAsnGluLeuProLysAsnGly 308
              |||:::||||
Db      2339  AAGCAAGAAACTAGTATGATTTGGTAGTGAAGAAACAAAGTGAG----- 2383
              |||:::||||
QY      309  LysGlySerThrArgLysGlyValAspHisSerAsnArgAsnGlnAlaThrLeuAsnGlu 328
              |||:::||||
Db      2384  -----ACTGCTCCAAAGGGTCAACACAGGAGCGAGGAACCAATACAAATGAGTGAA 2437
              |||:::||||
QY      329  LysGlnArg-----PheProSerLysGlyLysSer 338
              |||:::||||
Db      2438  AAGAAGCGCCTCTGCGAGATAAGAAAGCACAGAGACCAATTTGAACGAGTGACTTTCT 2497
              |||:::||||
QY      339  GlnGlyLeuProLysProSerArgGlyLeuAspAsnGluLeuLysAsnGluMetAspSer 358
              |||:::||||
Db      2498  GACAGCATAAATTCAGACTCCAGATTAGGTGAAGTGTTCAGAAATAAGATTCTGAT 2557
              |||:::||||
QY      359  Phe-----AsnGlyProSerHisGluAsnLeuThrHisGlyArgLysTyrHisTyr 376
              |||:::||||
Db      2558  TATCTGAAGAACACACACCTGAGGACATCTGAAGACCTCAGCGGCT----- 2605
              |||:::||||
QY      377  ValProHisArgGlnAsnAsnSerThrArgAsnLysGlyMetProGlnGlyLysGlySer 396
              |||:::||||
Db      2606  -----GCAGGGGAGCCTCAGGGAGAACTCTCA 2632
              |||:::||||
QY      397  TrpGlyArgGlnProHisSerAsnArgArgPheSerSerArgArgAspAspSerSer 416
              |||:::||||
Db      2633  -----AAGAGGACCATGAGAAC-----ACAGAGAAGTACATGCGGCACA 2671
              |||:::||||
QY      417  GluSerSerAspSerGlySerSerSerGluSerAsp 428
              |||:::||||
Db      2672  GAAAGCCAGGGTCTGCTGCTGCAGAACCTGAAGAT 2707
              |||:::||||

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RESULT 12

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US-10-153-668-301
; Sequence 301, Application US/10153668
; Publication No. US20030092616A1
; GENERAL INFORMATION:
; APPLICANT: HONDA, Goichi
; APPLICANT: MATSUDA, Akio
; APPLICANT: MURAMATSU, Shuji
; APPLICANT: ISHIZAWA, Kenya
; TITLE OF INVENTION: STAT6 Activating Gene
; FILE REFERENCE: 1254-0207P
; CURRENT APPLICATION NUMBER: US/10/153,668
; PRIORITY FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: US 60/293,172
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/316,031
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/328,403
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: JP 2001-157043
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: JP 2001-260681
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: JP 2001-313175
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 488

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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 301
; LENGTH: 2673
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (33)..(2348)
US-10-153-668-301

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Alignment Scores:

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Pred. No.: 0.000862 Length: 2673
Score: 140.00 Matches: 87
Percent Similarity: 32.08% Conservative: 49
Best Local Similarity: 20.52% Mismatches: 144
Query Match: 6.14% Indels: 144
DB: 14 Gaps: 17

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US-09-700-696C-2 (1-430) x US-10-153-668-301 (1-2673)

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QY      23  ProLysSerThrGlyAsnLysGlyPheGluAspGlyAspAspAlaIleSerLysLeuHis 42
              |||:::||||
Db      660  CCTGGGAAGGCCACAGCAATGCTTTTCAGACAGACTCGGGCCAGCCAGACGACAC 719
              |||:::||||
QY      43  AspGlnGluGluTyrGlyAlaAlaLeuLeuArgAsnAsnMetGlnHisIleMetGlyPro 62
              |||:::||||
Db      720  CTGGGTGAACCCCATCGGAAGGGTGTGTGAGTCAAAACAAAGAGGAC----- 767
              |||:::||||
QY      63  ValThrAlaIleLysLeuGluGluAsnLysGluAsnThrProArgAsnValLeu 82
              |||:::||||
Db      767  -----
QY      83  AsnIleProAlaSerMetAsnTyrAlaLysAlaHisSerLysAspLysLysLysPro 102
              |||:::||||
Db      768  -----AAATCTCCCAAGAGCAAAACGCCCGTG 797
              |||:::||||
QY      103  GlnArgAspSerGlnAlaGlnLysSerProValLysSerLysSerThrHisArgIleGln 122
              |||:::||||
Db      798  GATGCCAAGAGTGATGAGAAGGCTCTGTGTGTCAGCAGAGAGAAATCACAC----- 848
              |||:::||||
QY      123  HisAsnIleAspTyrLeuLysHisLeuSerLysValLysLysIleProSerAspPheGlu 142
              |||:::||||
Db      849  -----AAGGCCCTCTCCAAA----- 863
              |||:::||||
QY      143  GlySerGlyTyrThrAspLeuGlnGluArgGlyAspAsnAspIleSerProPheSerGly 162
              |||:::||||
Db      864  -----GAGGAGAACCGAGGCCACCTCAGG 890
              |||:::||||
QY      163  AspGlyGlnProPheLysAspIleProGlyLysGlyGluAlaThrGlyProAspLeuGlu 182
              |||:::||||
Db      891  GACAAATGCAAGGGAGAAACCG---CCCTCTAGTGGGTAAAGAAAGAGAGAGACAGAG 947
              |||:::||||
QY      183  GlyLysAspIleGlnThrGlyPheAlaGlyProSerGluAlaGluSer---ThrHisLeu 201
              |||:::||||
Db      948  GCAGCAGCCTGAAGAGAGTGTGTGCTCCTCTAGAGCGCTTCAGAACCAACCTG 1007
              |||:::||||
QY      202  AspThrLysLysProGlyTyrAsnGluIleProGluArgGluGluAsnGlyGlyAsnThr 221
              |||:::||||
Db      1008  -----AAAAAGCCAAAGCACAGAGAC---CCAGAGAAAGCCCAA----- 1043
              |||:::||||
QY      222  IleGlyThrArgAspGluThrAlaLysGluAlaAspAlaValAspValSerLeuValGlu 241
              |||:::||||
Db      1044  -----TTGGACAAAAGCAAGCAAGTCTGGACAGCTTTGACACAGGA-----AAA 1088
              |||:::||||
QY      242  GlySerAsnAspIleMet-----GlySerThrAsnPheLysGluLeu 255
              |||:::||||
Db      1089  GGAGCAGAGAGCTGTGCCCCAGGTAAAGAGAGAGGGTCTTAAACACTAAGACTCCA 1148
              |||:::||||
QY      256  ProGlyArgGluGlyAsnArgValAspAlaGlySerGlnAsnAlaHisGlnGlyLysVal 275
              |||:::||||
Db      1149  GAAAGGAAAGTCAAAACCTAAATTTGGATAGAAAGTCACTGGGGCTCC---CTCCCTAAAGTT 1205
              |||:::||||
QY      276  -----GluPheHisTyrPro----- 280
              |||:::||||

```

```
Db 1206 GAGGAGACAGATATGAGGATGAATTCAGACAGCCAAACCATGTCTTTTGAATCTACTC 1265
Qy 281 -----ProAlaProSerLysGluLysArgLysGluGlySerAspAlaAlaGluSer 298
Db 1266 AGCTATGACACGCCCCGGAAGAAAAAGAAAGATTGTGAAACT---TCAGCCACGGCA 1322
Qy 299 ThrAsnTyrAsnGluLysProLysAsnGlyLysGlySerThrArgLysGlyValAspHis 318
Db 1323 CTTGGAGATAAAGACTTAAAAAATGACTCTTAAAGCACTGTGTAATAAACTTGCACTCA 1382
Qy 319 SerAsnArgAsnGlnAlaThrLeuAsnGluLysGlnArgPheProSerLysGlyLysSer 338
Db 1383 GTTCAGAAATACCCAGAGTGAACAAACCAAGTCAGAGAGCCGCTGGAGCTGATTTA 1442
Qy 339 GlnGlyLeu----- 341
Db 1443 GCCAAGCTGAGAAAGTGCCGTGATGTGTCAGTGTTCAGACCTCCCGTTACCCGCG 1502
Qy 342 -----ProIleProSerArgGlyLeuAspAsnGluLysLeuAsnGlu 355
Db 1503 ATACAGCCCAATTACCGTCCACTCCCTCCCTCGAGCTGATATCCTCTCCAGCCAAAG 1562
Qy 356 MetAspSerPheAsnGlyProSerHisGluAsn----- 366
Db 1563 CGAAAGCGTCTCTTCCACCCCGAAGAAAGAAAGAGTGGATTACTGGCGCAGATG 1622
Qy 367 -----IleIleThrHisGlyArgLysTyrHisTyrValPro----- 378
Db 1623 AATTCCAAGATGACGAGTGTCTCTGTTCCAGGTGCTCTATCTCTCCCTAAATATGATGACC 1682
Qy 379 ---HisArgGln 381
Db 1683 TTGCACACAGCAA 1694
```

RESULT 13

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US-10-101-510-398
; Sequence 398, Application US/10101510
; Publication No. US20030148295A1
; GENERAL INFORMATION:
; APPLICANT: WAN, JACKSON
; APPLICANT: WANG, YIXIN
; TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE
; FILE REFERENCE: 15117.0012
; CURRENT APPLICATION NUMBER: US/10/101,510
; CURRENT FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: 60/276,947
; PRIOR FILING DATE: 2001-03-20
; NUMBER OF SEQ ID NOS: 805
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 398
; LENGTH: 4839
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (3080)..(3102)
; OTHER INFORMATION: a, t, c, g, other or unknown
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (4828)
; OTHER INFORMATION: a, t, c, g, other or unknown
US-10-101-510-398
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Alignment Scores:
Pred. No.: 0.00187 Length: 4839
Score: 140.00 Matches: 87
Percent Similarity: 32.08% Conservative: 49
Best Local Similarity: 20.52% Mismatches: 144
Query Match: 6.14% Indels: 144
DB: 12 Gaps: 17
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US-09-700-696C-2 (1-430) x US-10-101-510-398 (1-4839)

```
Qy 23 ProLysSerThrGlyAsnLysGlyPheGluAspGlyAspAlaIleSerLysLeuHis 42
Db 663 CTGGGAAAGCCACAGCAATGCTTTTCAGCAGACAGCTCGGGGCCAGCAAGACGACAC 722
Qy 43 AspGlnGluGluTyrGlyAlaLeuLeuArgAsnAsnMetGlnHisIleMetGlyPro 62
Db 723 CTGGGTGAACCCCATGGGAAAGGGGTTGTGAGTCAAAACAGAGACAC----- 770
Qy 63 ValThrAlaIleLysLeuGluLysGluAsnLysGluAsnThrProAsnValLeu 82
Db 770 ----- 770
Qy 83 AsnIleProAlaSerMetAsnTyrAlaLysAlaHisSerLysAspLysLysLysPro 102
Db 771 -----AAATCTTCCCAAGGACAAACGCCCGCTG 800
Qy 103 GlnArgAspSerGlnAlaGlnLysSerProValLysSerLysSerThrHisArgIleGln 122
Db 801 GATGCCAAGAGTGATGAGAAAGGCTCTGTGTGAGCAGAGAGAAATCACAC----- 851
Qy 123 HisAsnIleAspTyrLeuLysHisLeuSerLysValLysLysIleProSerAspPheGlu 142
Db 852 -----AAGGCCCTCTCCAA----- 866
Qy 143 GlySerGlyTyrThrAspLeuGlnGluArgGlyAspAsnAspLysSerProPheSerGly 162
Db 867 -----GAGGAGAAACCGAAGGCCACCTCAGG 893
Qy 163 AspGlyGlnProPheLysAspIleProGlyLysGlyGluAlaThrGlyProAspLeuGlu 182
Db 894 GACAATGCAAGGGAGAAACCG---CCCTCTAGTGGGTAAAGAAAGAGAGGACAGAGAG 950
Qy 183 GlyLysAspIleGlnThrGlyPheAlaGlyProSerGluAlaGluSer---ThrHisLeu 201
Db 951 GGCAGCAGCTGAAGAAGAGTGTTCCTCCCTCAGAGCCGCTTCAGACCAACCACTG 1010
Qy 202 AspThrLysLysProGlyTyrAsnGluLysProGluArgGluGluAsnGlyGlyAsnThr 221
Db 1011 -----AAAAAGCCAAAGCACAGAGAC---CCAGAGAAAGCCCAA----- 1046
Qy 222 IleGlyThrArgAspGluThrAlaLysGluAlaAspAlaValAspValSerLeuValGlu 241
Db 1047 -----TTGACAAAGCAAGCAAGGTCTGACAGCTTTTCACACAGCA-----AAA 1091
Qy 242 GlySerAsnAspIleMet-----GlySerThrAsnPheLysGluLeu 255
Db 1092 GGAGCAGGAGACCTGTGCCCAGGTAAAGAGAGAGGTTCTAACACCTTAAGACTCCA 1151
Qy 256 ProGlyArgGluGlyAsnArgValAspAlaGlySerGlnAsnAlaHisGlnGlyLysVal 275
Db 1152 GAAGGGAAAGTCAAAACTAATTGATAGAAAGTCACTGGGCTCC---CTCCCTAAAGTT 1208
Qy 276 -----GluPheHisTyrPro----- 280
Db 1209 GAGGACAGATATGAGGATGAATTCGAGACGCCCAACCATGTCTTTGAATCCTACTC 1268
Qy 281 -----ProAlaProSerLysGluLysArgLysGluGlySerSerAspAlaAlaGluSer 298
Db 1269 AGCTATGACACGCCCCGGAAGAAAAAGAAAGATTGTGAAACT---TCAGCCACGGCA 1325
Qy 299 ThrAsnTyrAsnGluLysProLysLysGlyLysGlySerThrArgLysGlyValAspHis 318
Db 1326 CTTGGAGATAAAGGACTTAAAAAATGACTCTAAAGCACTGGTAAAAAATCTGGACTCA 1385
Qy 319 SerAsnArgAsnGlnAlaThrLeuAsnGluLysGlnArgPheProSerLysGlyLysSer 338
Db 1386 GTTCAGAAATACCCAGAGTGAACAAACCAAGTCAGAGAGCCGCTGGAGCTGATTTA 1445
Qy 339 GlnGlyLeu----- 341
Db 1446 GCCAAGCTGAGAAAGGTGCTGATGTGTGCCAGTGTTCACAGACCTCCCGTTACCCGCG 1505
```

```
QY 342 -----ProIleProSerArgGlyLeuAspAsnGluIleLysAsnGlu 355
Db 1506 ATACAGCCCAATTAACCTCCACTCCCTCCCTGAGCTGATATCTCTTCCAGCCAAAG 1565
QY 356 MetAspSerPheAsnGlyProSerHisGluAsn----- 366
Db 1566 CGAAAGCGTCTCTTCCACCCAGGAAGAAGAAAGCTGGATTACTGGCGCAGAAATG 1625
QY 367 -----lleIleThrHisGlyArgLysTyrHisTyrValPro----- 378
Db 1626 AATTCCAAAGTGCAGGTGTTACTGTTCCAAAGTGTGCTATCTCTCCCTAAATGATGACC 1685
QY 379 ---HisArgGln 381
Db 1686 TTGCACCAGCAA 1697

RESULT 14
US-10-161-572-6
; Sequence 6, Application US/10161572
; Publication No. US20030087266A1
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: IGS AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE
; FILE REFERENCE: EX02-097C-PC
; CURRENT FILING DATE: 2002-06-03
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/296,076
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/328,605
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/338,733
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US 60/357,253
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US 60/357,600
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-161-572-6

Alignment Scores:
Pred. No.: 0.0314 Length: 35465
Score: 139.00 Matches: 105
Percent Similarity: 37.87% Conservative: 48
Best Local Similarity: 25.99% Mismatches: 162
Query Match: 6.10% Indels: 93
DB: 14 Gaps: 17

US-09-700-696C-2 (1-430) x US-10-161-572-6 (1-35465)

QY 74 LysGluAsnThrProArgAsnValLeuAsnIleIleProAlaSerMetAsnTyrAlaLys 93
Db 881 AAACCAAGCAGACATCCCGTAACTCAGTC---ATGAGCCCAAGCAGTTCCTCCAGTCCACAA 937
QY 94 AlaHisSerLysAspLysLysProGlnArgAspSerGlnAlaGlnLysSerProVal 113
Db 938 TCGACCAAGTACAAAAGAGAGCCCTTCTAAACCGCCAGCAGCAGGTCCTCCG-AGTCCGCAG 996
QY 114 LysSerLysSerThrHisArgIleGlnHisAsnIleAspTyrLeuLysHisLeuSerLys 133
Db 997 CAAAGCAAGAACACCCAGCAGGGGTGAGCAC-----CCACACCAAGGACCAG 1041
QY 134 ValLysLysIleProSerAspPheGluGlySerGlyTyrThrAspLeuGlnArgGly 153
Db 1042 -----CAAAGCCAGCAAGGCCAG 1059
QY 154 AspAsnAspIleSerProPheSerGlyAspGlyGlnProPheLysAspIleProGlyLys 173
Db 1060 CGACGTGATGATCCACCAAGCGAGGGGCACACACAGCCGGGTAGGACACCTG-GCAGAA 1118
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QY 174 GlyGluAla-----ThrGlyProAspLeuGluGlyLysAspIle 186
Db 1119 GGGGAAGCCGAGCTTCCAAGAGGTCAACCAGCAGCGCCAGCACTCT-GGCAGG---ATA 1174
QY 187 GlnThrGlyPheAlaGlyProSerGluAlaGluSerThrHisLeuAspThr----- 203
Db 1175 AGAACTCATGTGTCAGACAGCAGCATGGCCAGCAGGAGTGAAGTCCCACTTCACAGCAA 1234
QY 204 -----LysLysProGlyTyrAsnGluIleProGluArgGluGluAsn--- 217
Db 1235 AAAGGGAGCCGGGAAGAGTTACGGCGGCTAGAACCCAGCAGCAAGGAAGAGGTGAC 1294
QY 218 -----GlyGlyAsnThrIleGly 223
Db 1295 AGCCAGCCTAGAAATCTGAGCAAGAGAGTTACCGCCCAACCAGGAGGCTCAGGTATAGG 1354
QY 224 ThrArgAspGlu-----ThrAlaLysGluAlaAspAlaValAspVal 237
Db 1355 AGGAGTTCAGAGTGGCTGTAACCTCCAGTAGTACAGCCCAAGTGTCAAACCCCGACTGGAATT 1414
QY 238 SerLeuValGluGlySerAsnAspIleMetGlySerThrAsnPheLysGlu----- 254
Db 1415 CCTCCAGGAGGAGAGTGTGACACCCATCTCCATCTCATCAAGGAAGGTGAAGAGTAC 1474
QY 255 -----LeuProGlyArgGlu-----GlyAsnArg 262
Db 1475 GGTCAAGATGATCATCCCGAGTAGGAAAGAGTTACAGCCCCACTGAAATGTCCAGCAGG 1534
QY 263 ValAspAlaGlySerGlnAsnAlaHisGlnGlyValGluPheHisTyrProPro--- 281
Db 1535 GTCAAGAGTTATAACACCAAGCCAGCAGCCCGCAGCAGCGCCGCAAAAGTCAAG-CCAATCTAG 1593
QY 282 AlaProSerLysGluLysArgLysGluGlySerSerAspAla-----AlaGluSerThr 299
Db 1594 AGCCCCAGAGAGTTCAGAGAGTGGCAGTCAAGAGAGACCAAGAGAGTGAAGAGTCA 1653
QY 300 AsnTyrAsnGluIleProLysAsnGlyLysGlySer-ThrArgLysGlyValAspHis 319
Db 1654 CAGTTGGAGAGAAACCATAGCAGGCGCAAGAGTCCGACCCCGAAGGGAATT----- 1705
QY 319 rAsnArgAsnGlnAlaThrLeuAsnGluLysGlnArgPheProSerLysGlyLysSerG 339
Db 1706 ----CTGAGCCAGATGGGAAGACACAGCCAGTCTAGAAGCCACAGCAAGCGGAAAGTCA 1761
QY 339 nGlyLeuPro---IleProSerArgGlyLeuAspAsnGluIleLysAsnGluMetAspSe 358
Db 1762 AAACCAATCTAGAACCCCGCAGAAAGAGAGAGTCAACTGTGCT----- 1807
QY 358 rPheAsnGlyProSerHisGluAsnIleIleThrHisGlyArgLysTyrHisTyrVal-- 377
Db 1808 ----AGAAACCCCGCAGCAAGGAAGAGTCTATAGTCCATTCAGAAAGTCCAGCAAGAGAG 1863
QY 378 -ProHisArgGlnAsnAsnSerThrArgAsnLysGlyMetProGlnGlyLysGlySerTr 397
Db 1864 AGATCAAGGGGATCTAGCAGCCCGCCAGGAGAGTGTGTCGAGTCAATCAGGAAGCCC 1923
QY 397 pGlyArgGln---ProHisSerAsnArgPheSerSerArgArgAspAspSerSe 416
Db 1924 CAAACAGCAGAGAGATCACAGCGATCTTAGAAGTCCCAACAGCGCAGAGATCGCAGCG 1983
QY 416 rGluSerSer 419
Db 1984 ATCTAGAGT 1993

RESULT 15
US-10-161-572-8
; Sequence 8, Application US/10161572
; Publication No. US20030087266A1
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: IGS AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE
; FILE REFERENCE: EX02-097C-PC
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